

Fig. 1

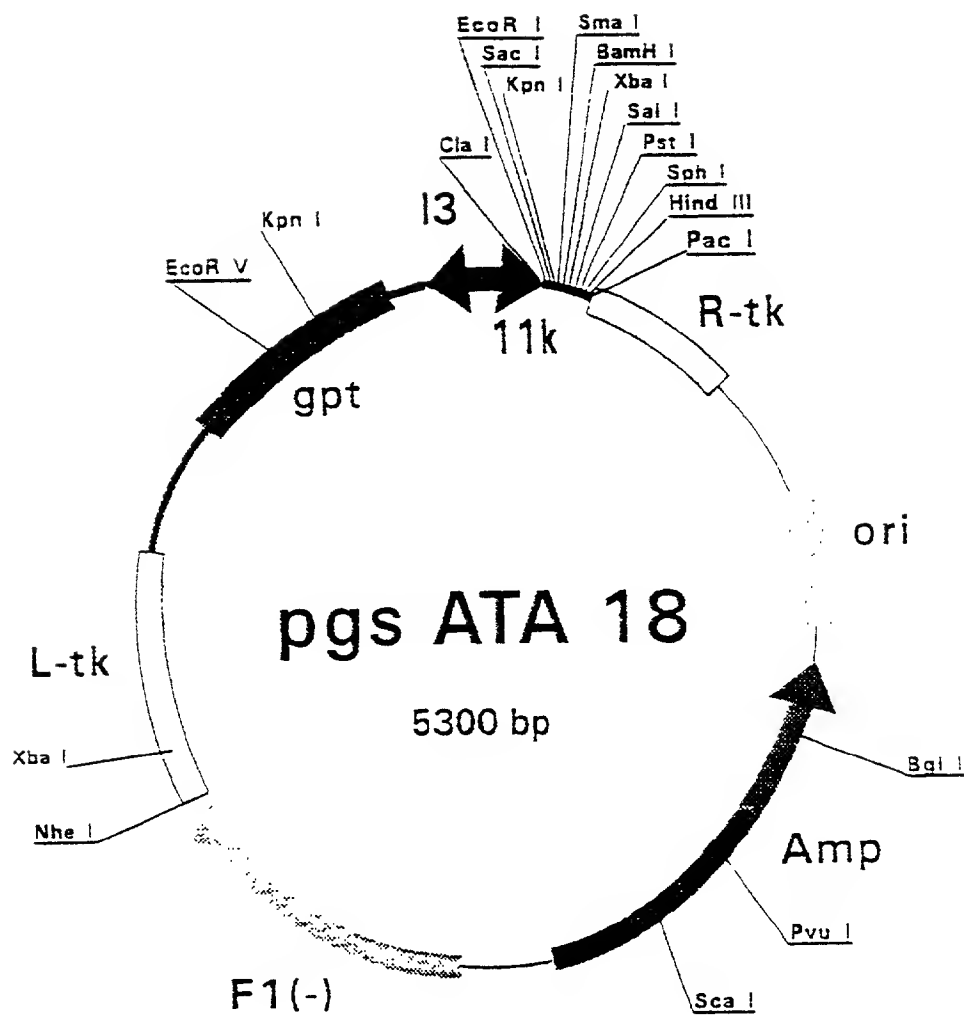


Fig. 2

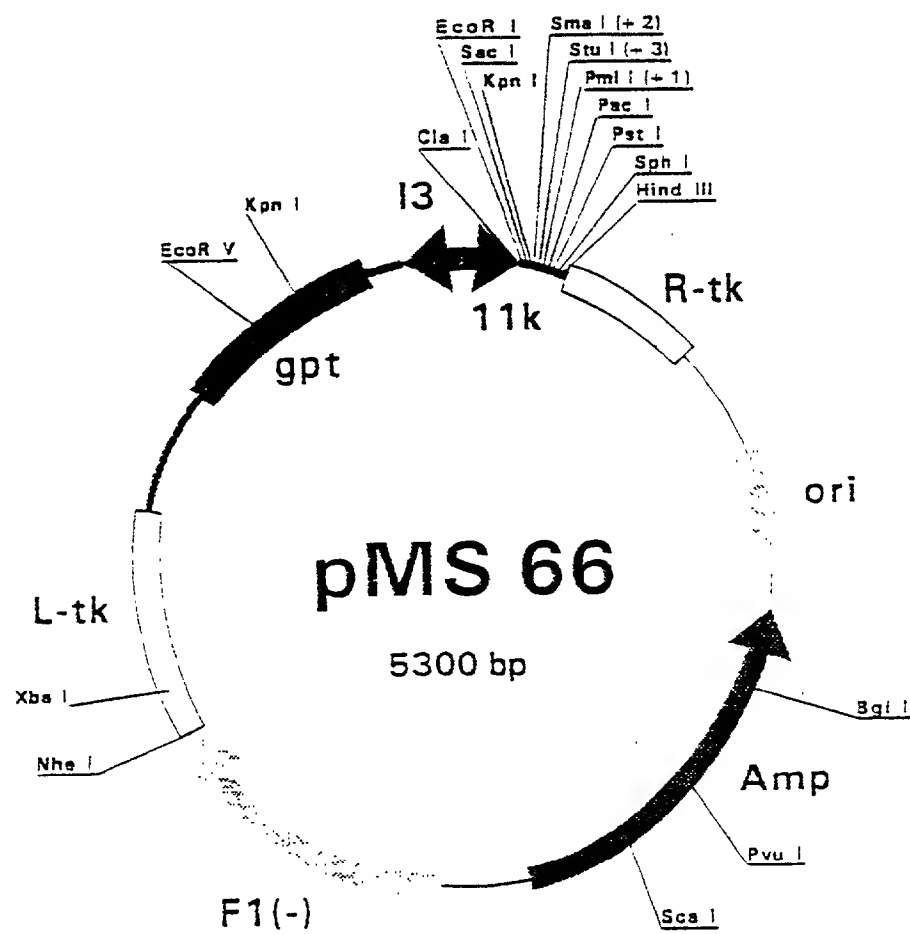


Fig. 3

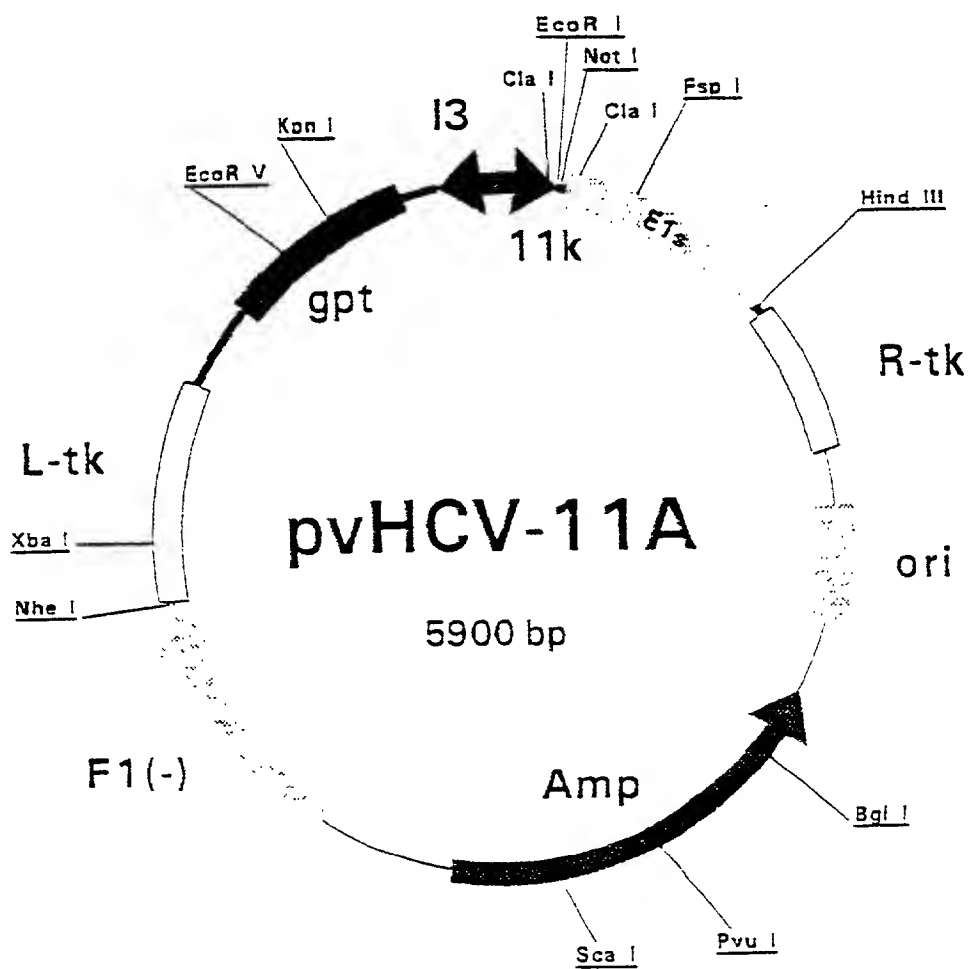
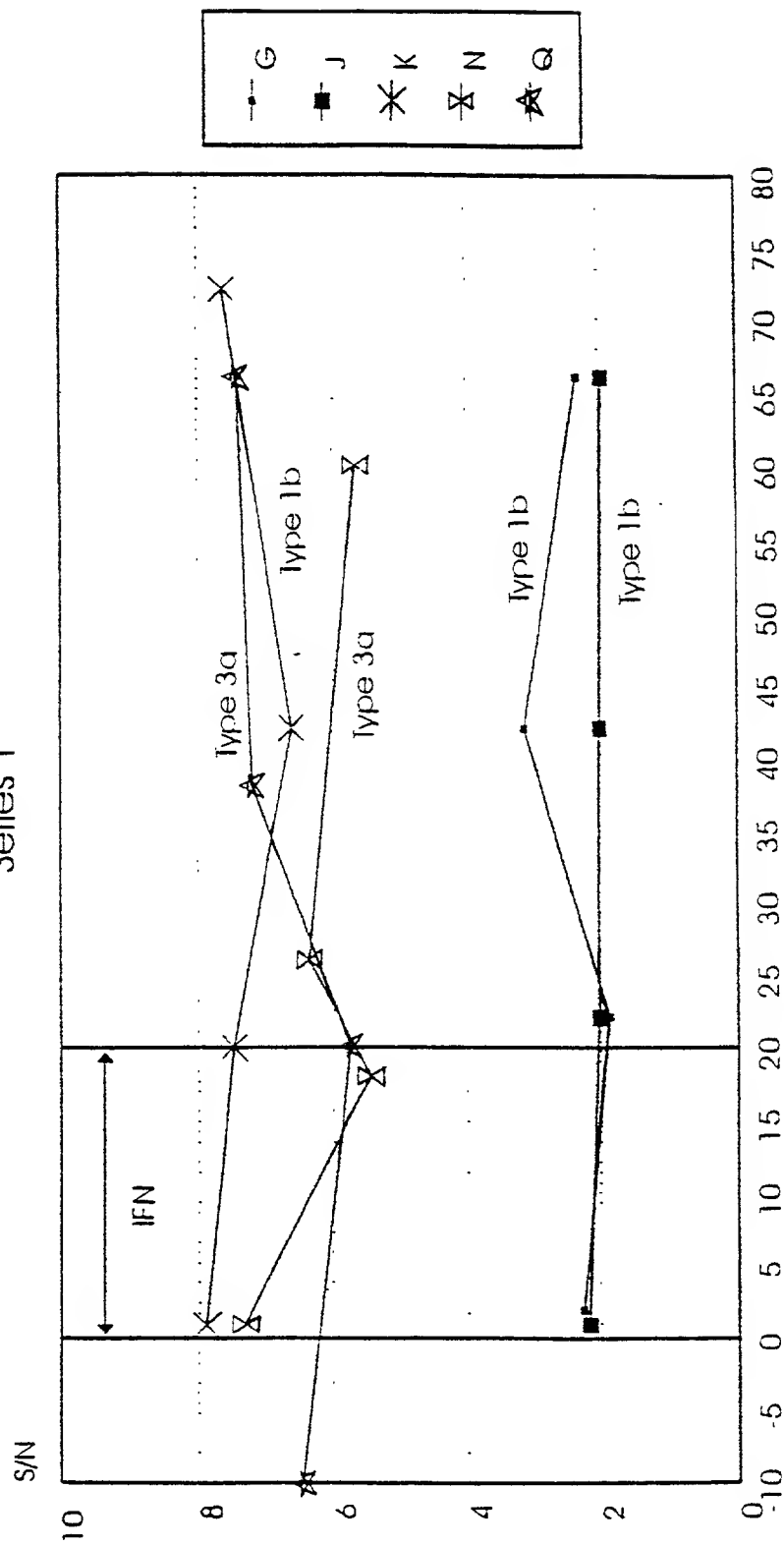


Fig. 4

Anti-E1 levels in NON-responders to IFN treatment

Series 1

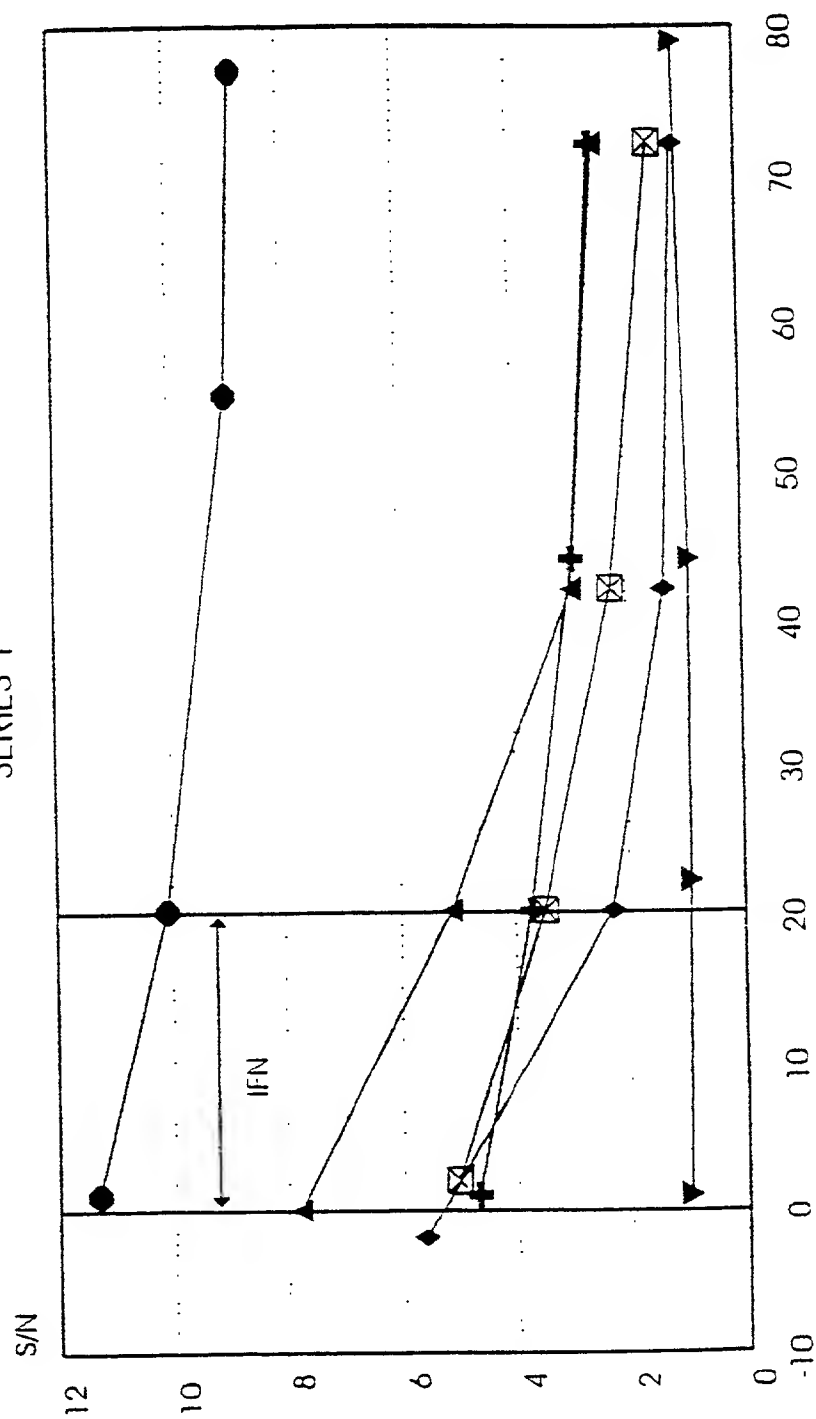


weeks after start of treatment

Fig. 5

Anti-E1 levels in RESPONDERS to IFN treatment

SERIES 1



weeks after start of treatment

Fig. 6

Anti-E1 levels in patients with COMPLETE response to IFN

SERIES 2

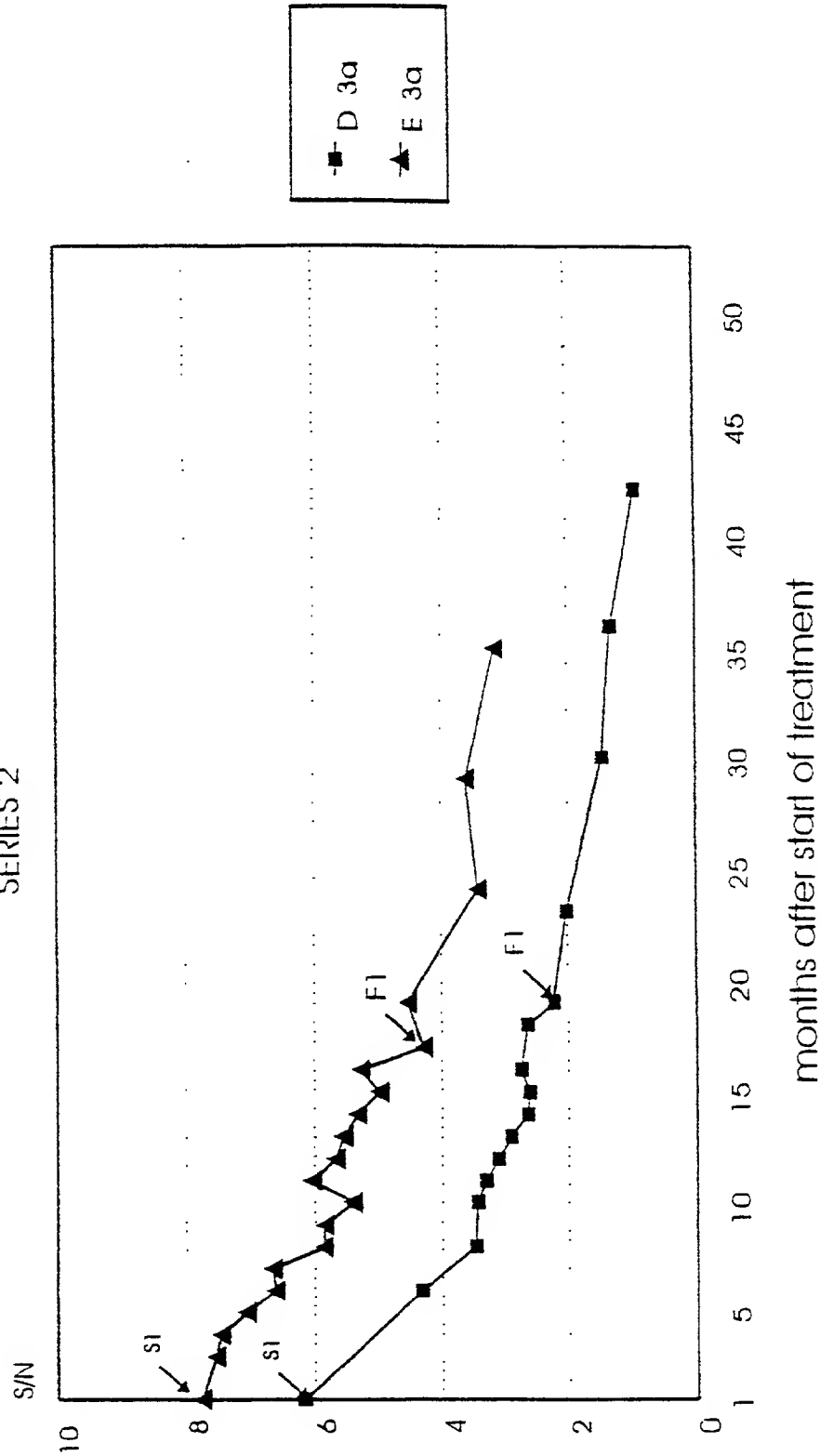
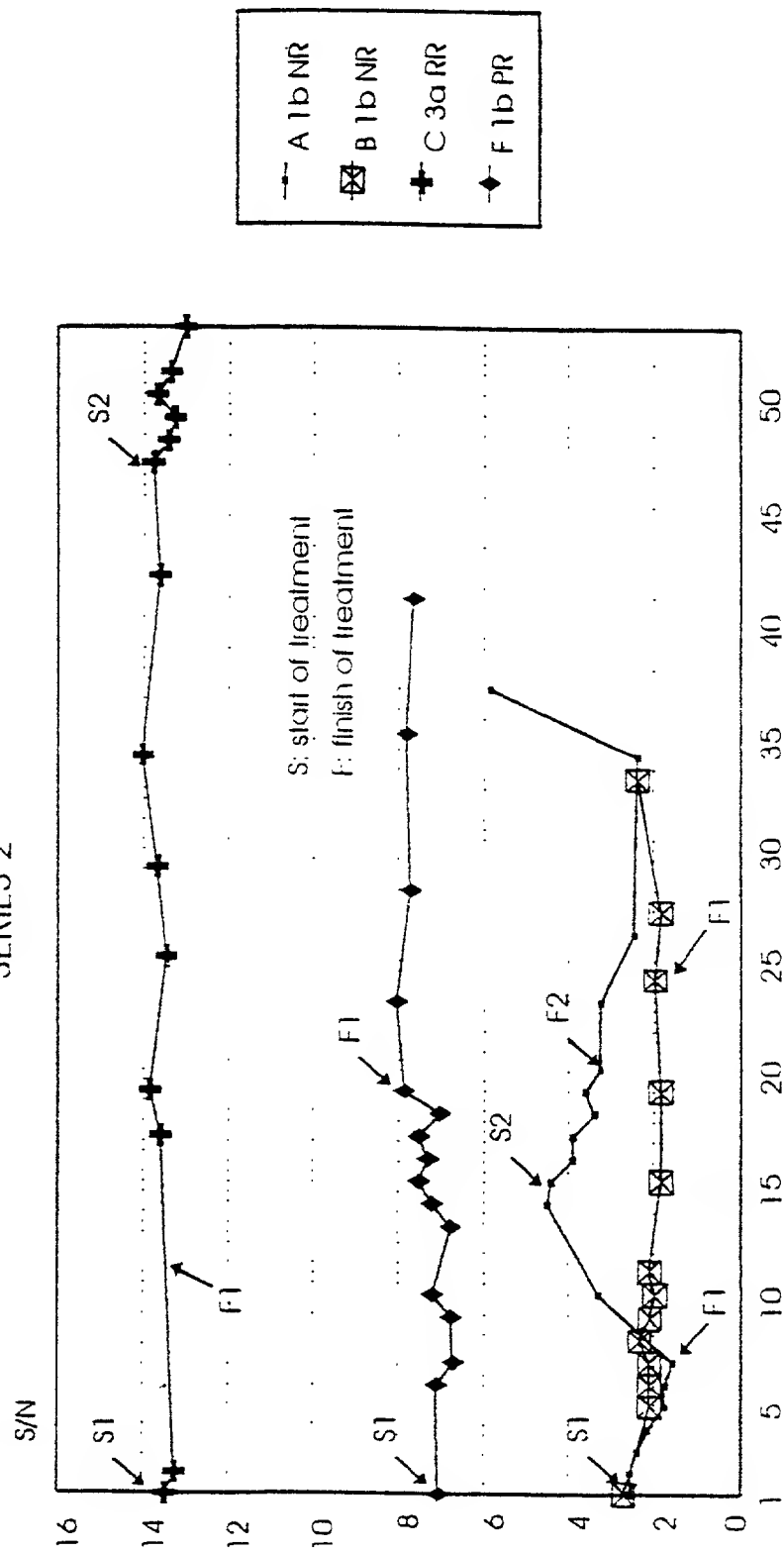


Fig. 7

Anti-E1 levels in INCOMPLETE responders to IFN treatment

SERIES 2

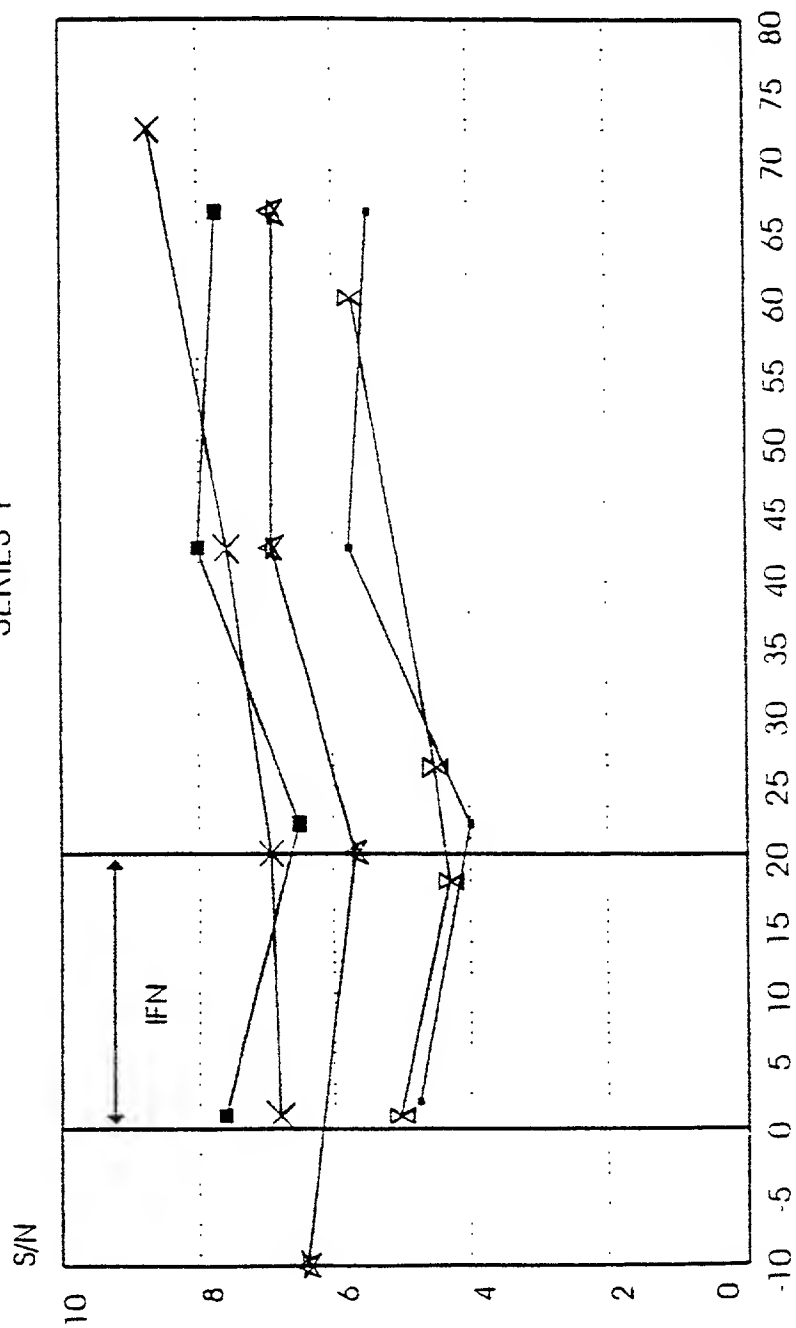


months after start of treatment

Fig. 8

Anti-E2 levels in NON-RESPONDERS to IFN treatment

SERIES 1

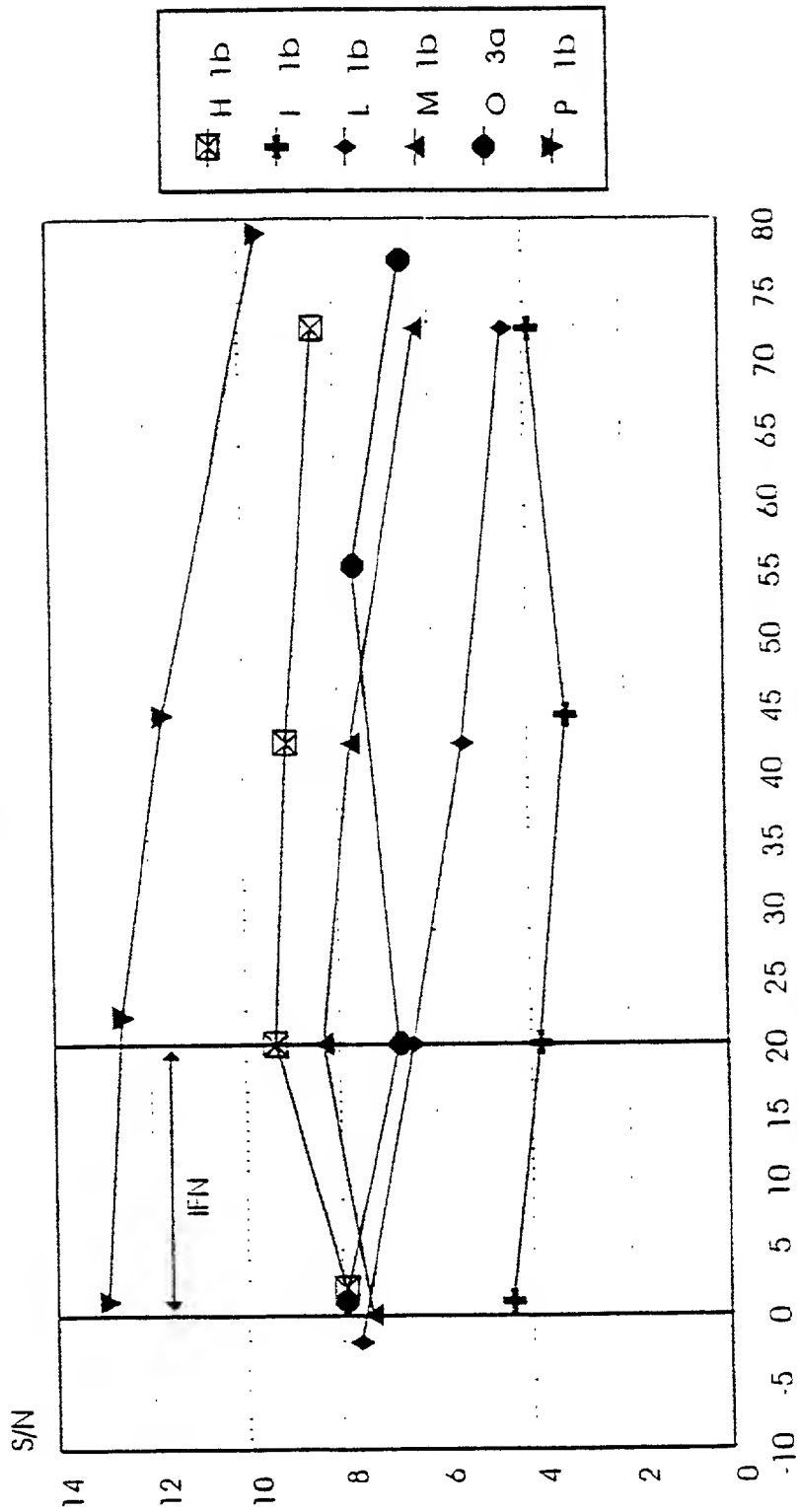


weeks after start of treatment

Fig. 9

Anti-E2 levels in RESPONDERS to IFN treatment

SERIES 1

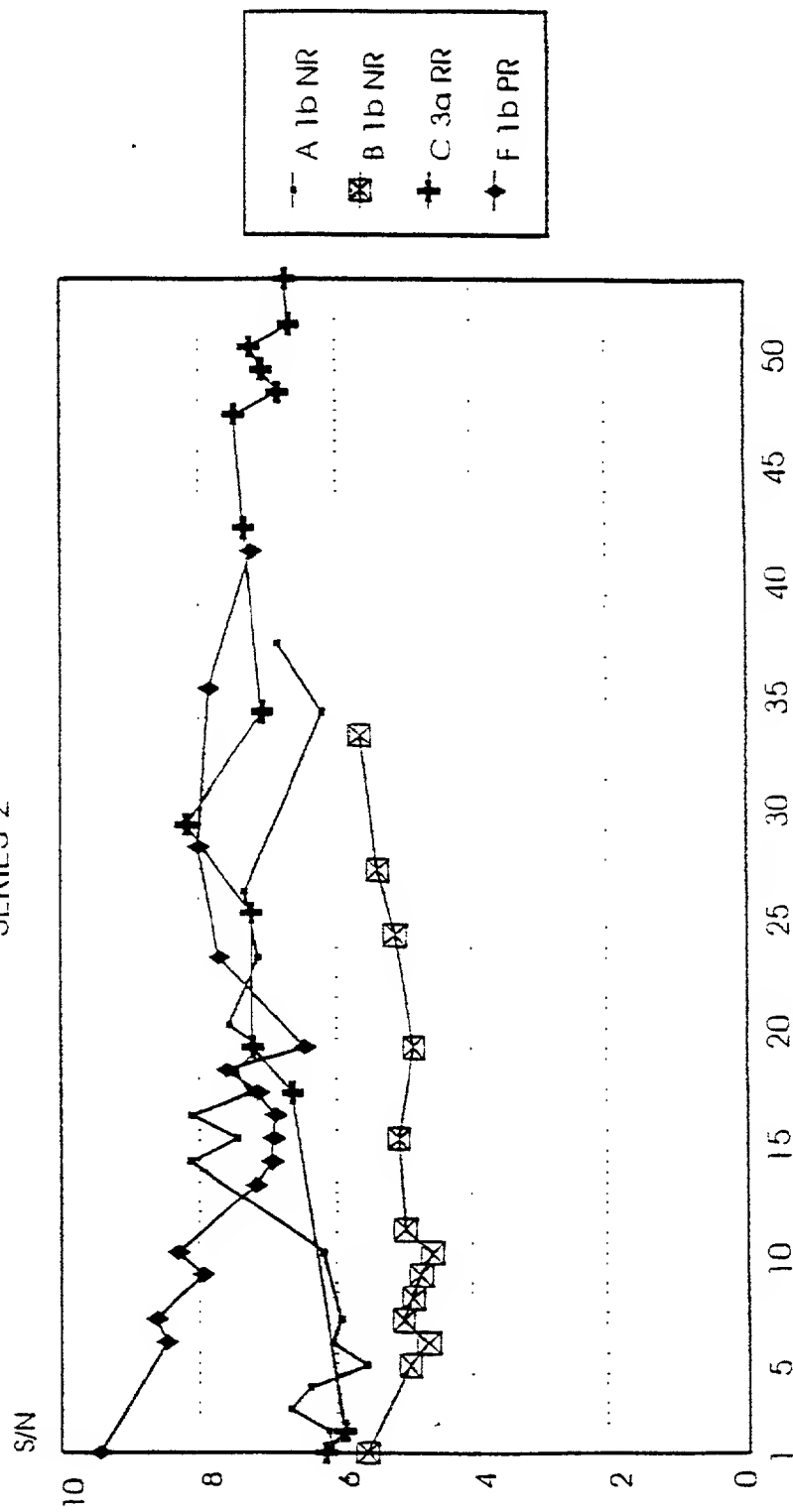


weeks after start of treatment

Fig.10

Anti-E2 levels in INCOMPLETE responders to IFN treatment

SERIES 2

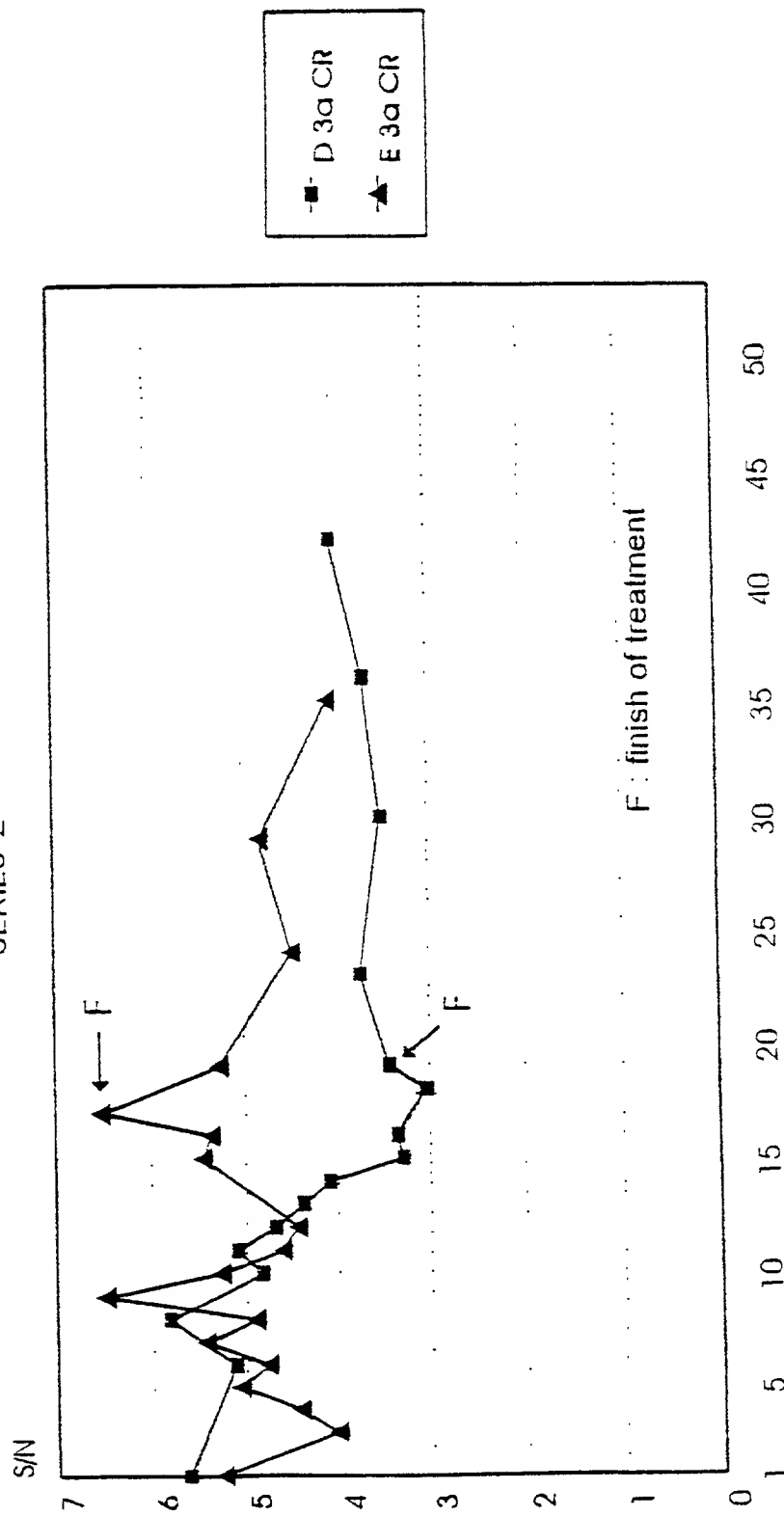


months after start of treatment

Fig.11

Anti-E2 levels in COMPLETE responders to IFN treatment

SERIES 2



months after start of treatment

Fig.12

Human anti-E1 reactivity competed with peptides

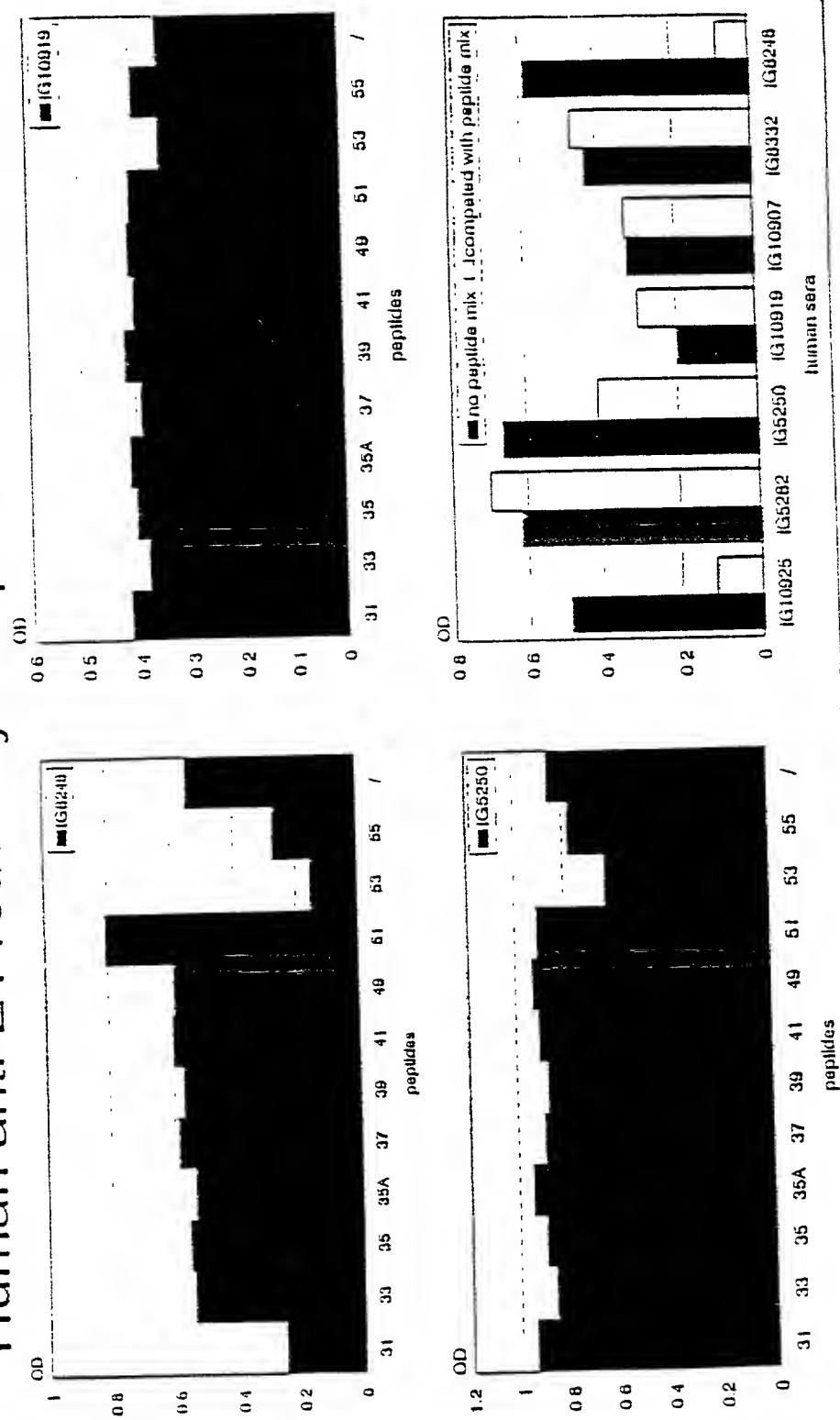


Fig.13

Competition of reactivity of anti-E1 Mabs with peptides

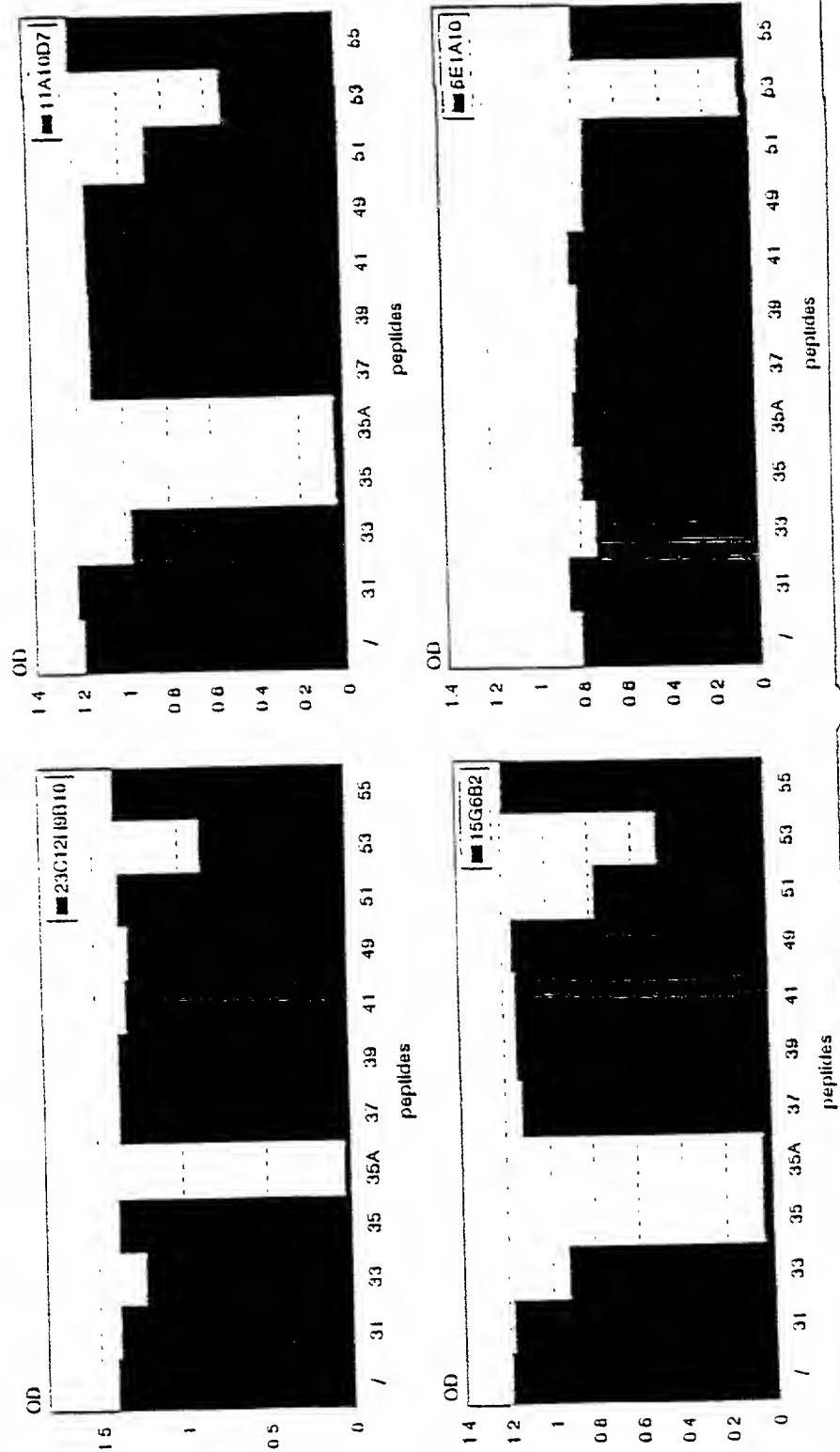


Fig.14

Anti-E1 (epitope 1) levels in NON-RESPONDERS to IFN treatment

SERIES 1

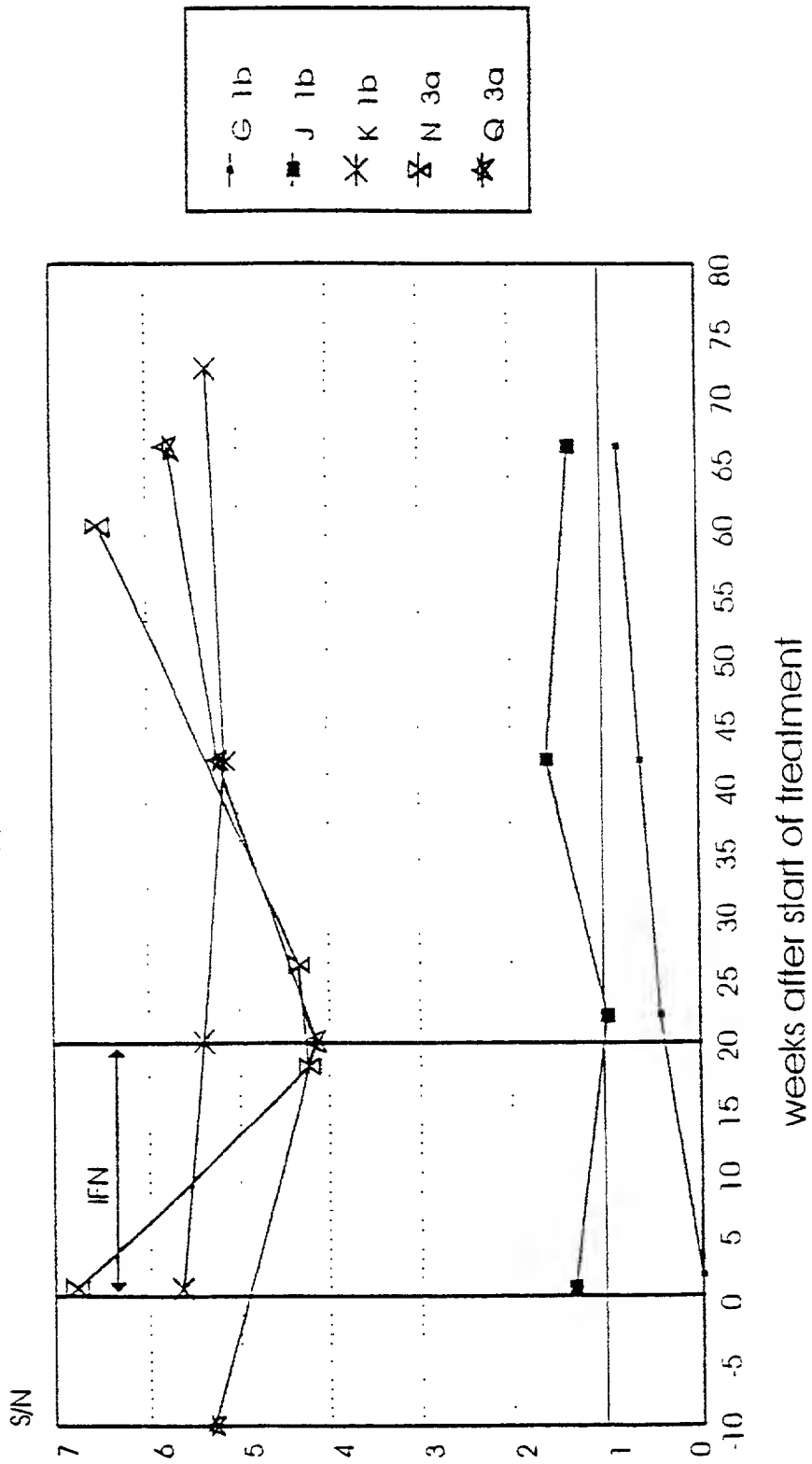
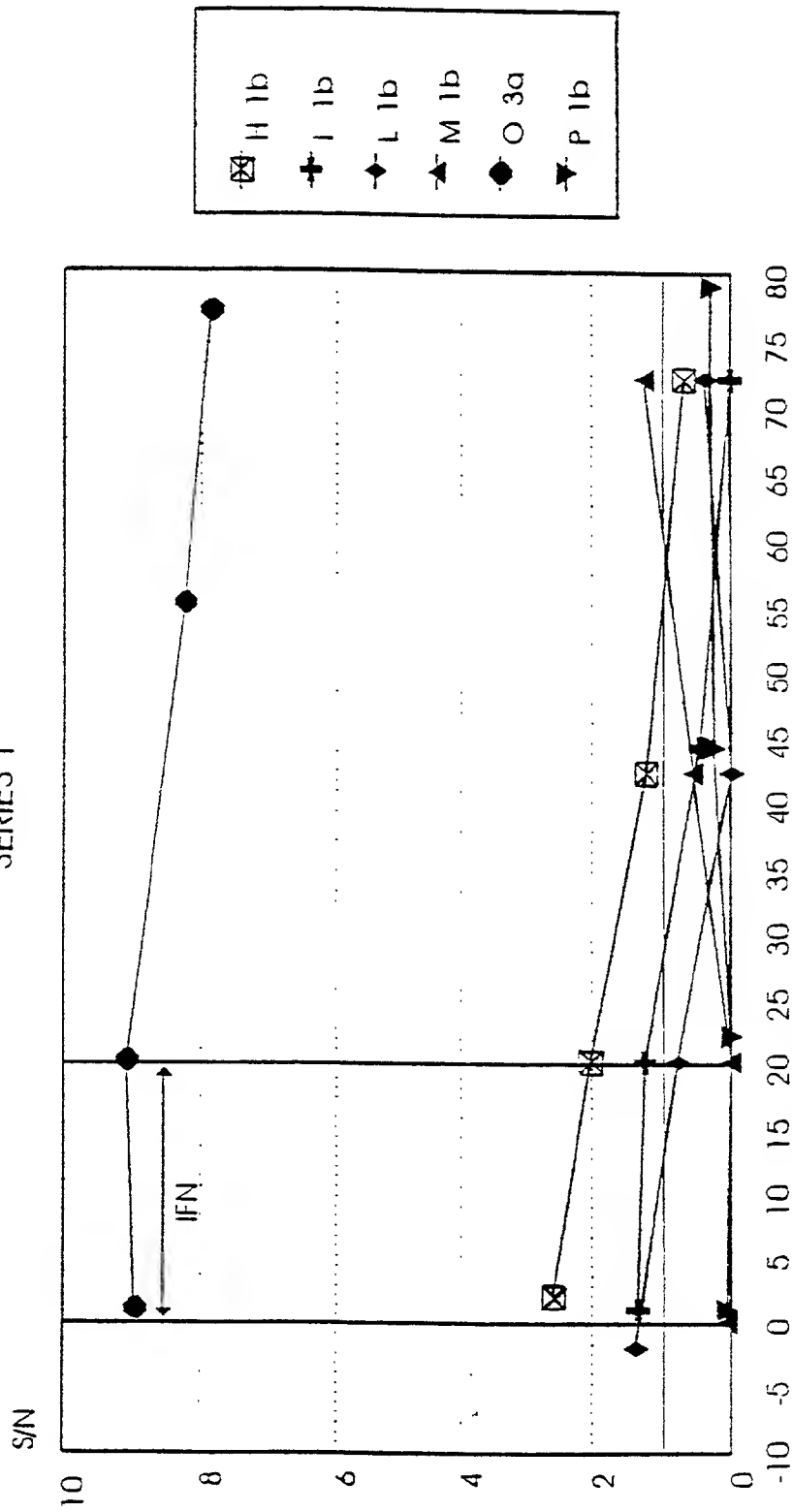


Fig.15

Anti-E1 (epitope 1) levels in RESPONDERS to IFN treatment

SERIES 1



weeks after start of treatment

Fig.16

Anti-E1 (epitope 2) levels in NON-RESPONDERS to IFN treatment

SERIES 1

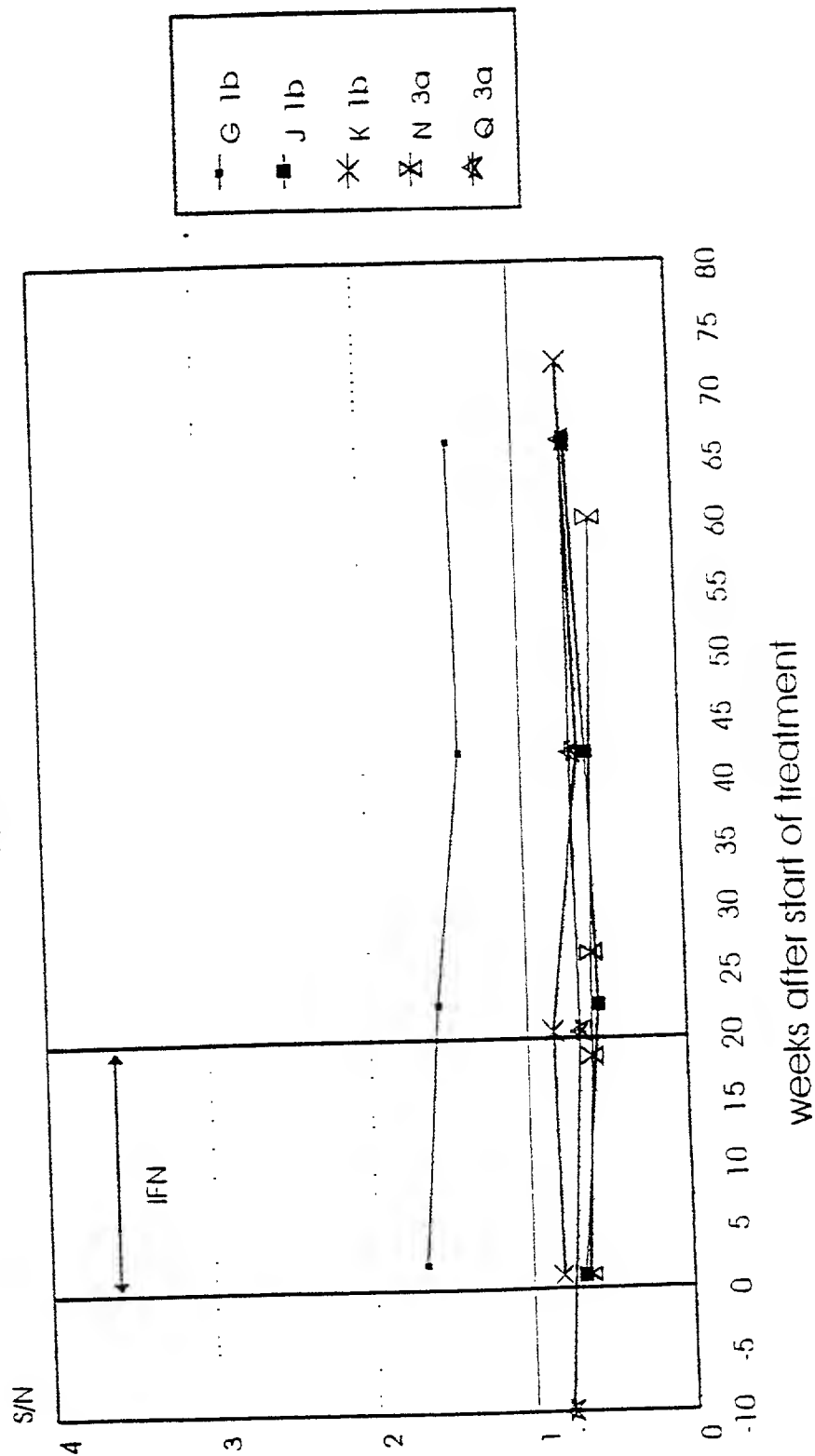
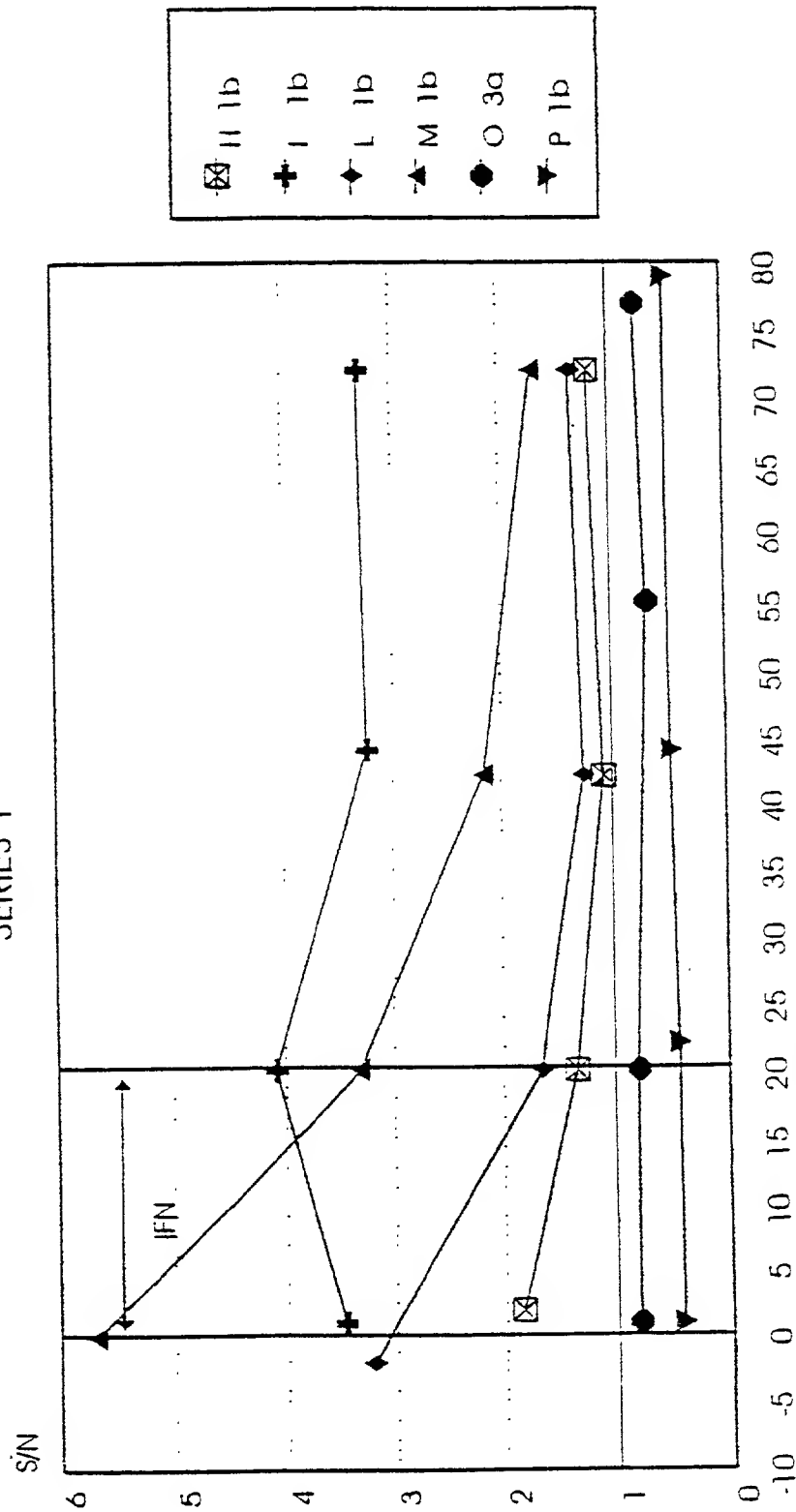


Fig.17

Anti-E1 (epitope 2) levels in RESPONDERS to IFN treatment

SERIES 1



weeks after start of treatment

Fig.18

Competition of reactivity of anti-E2 Mabs with peptides

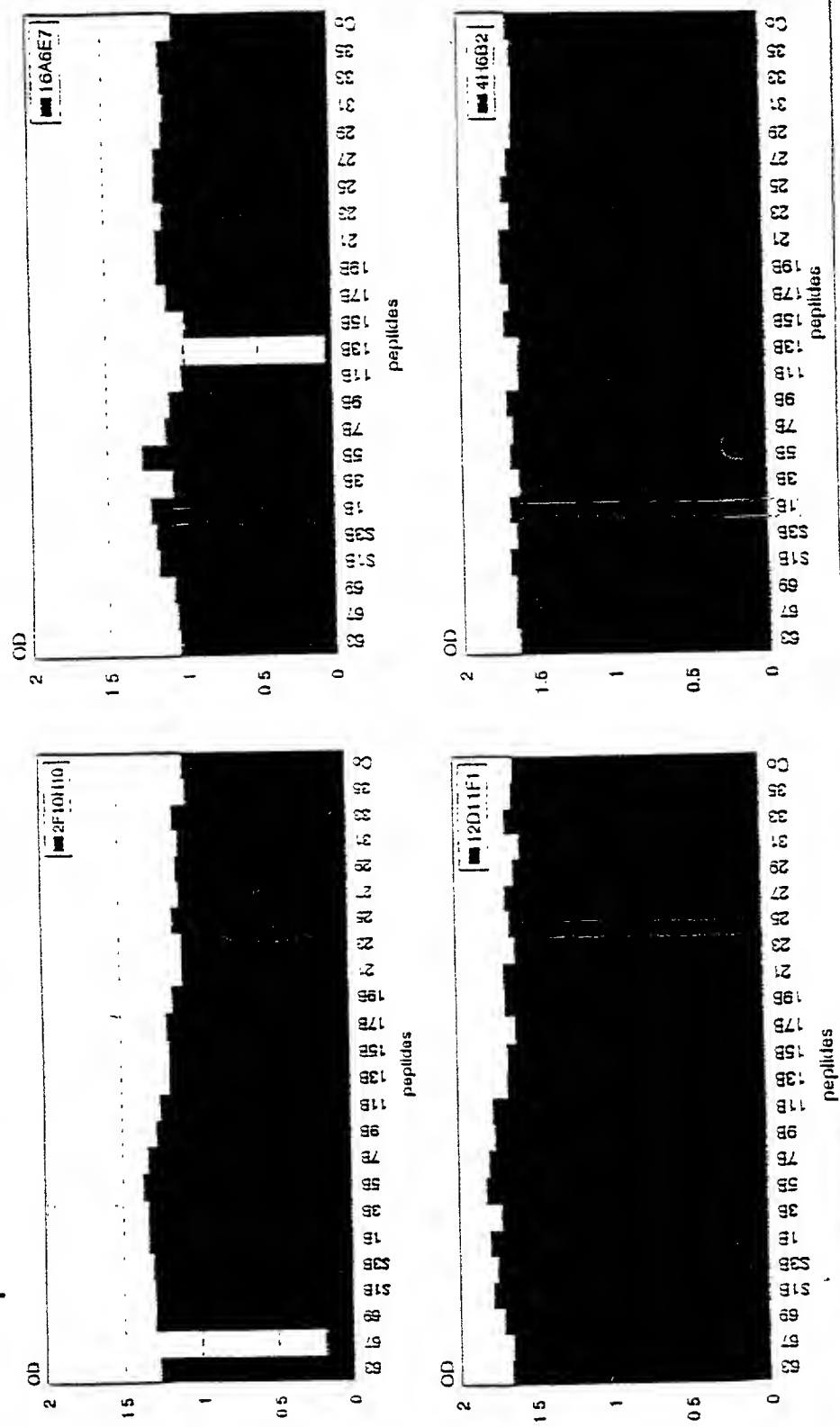


Fig.19

Human anti-E2 reactivity competed with peptides

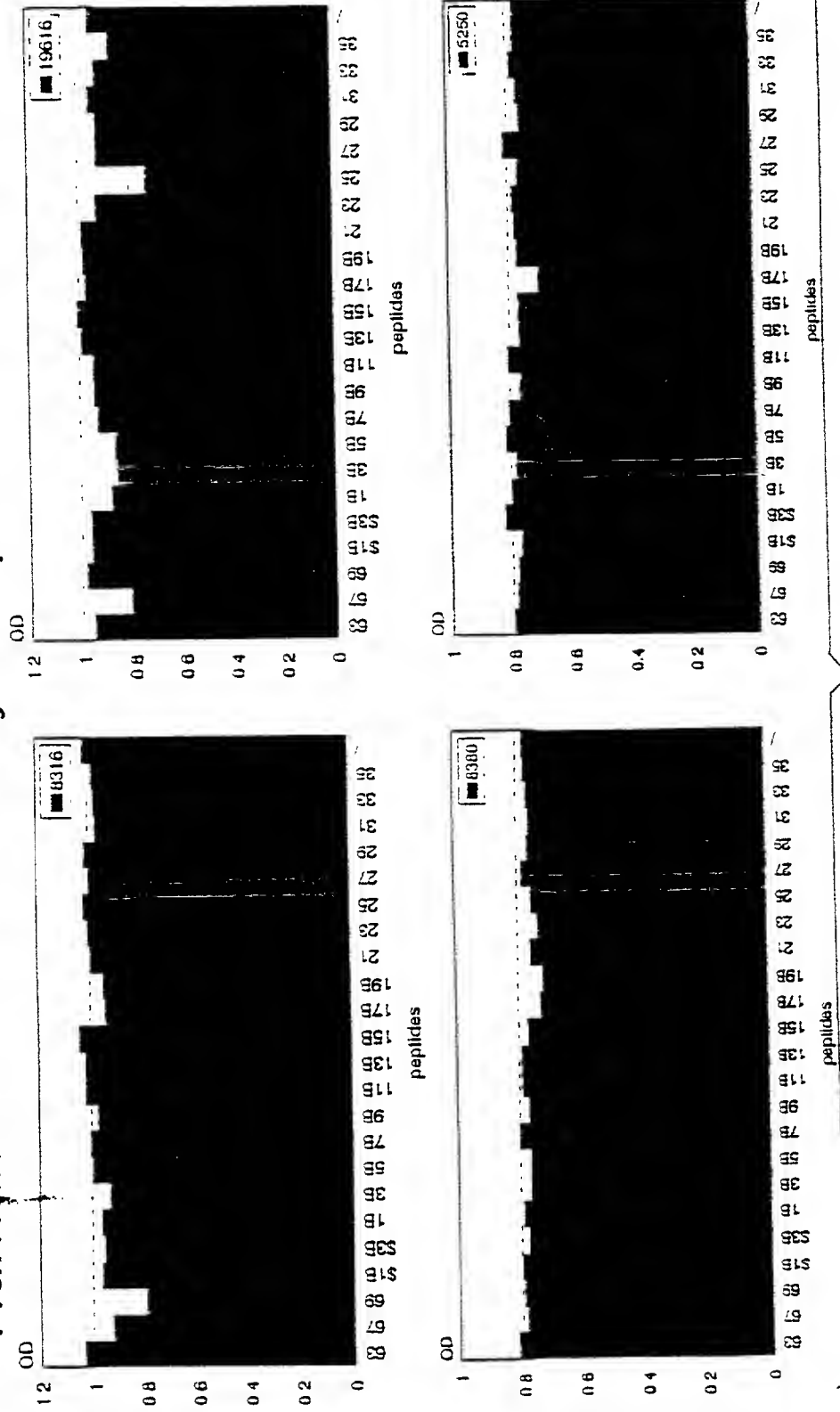


Fig. 20

Fig. 21A

5' GGCATGCAAGCTTAATTAATT3' (SEQ ID NO 1)

3'ACGTCCGTACGTTTGAATTAATTAATCGA5' (SEQ ID NO 94)

5'CCGGGGAGGCCTGCACGTGATCGAGGGCAGACACCATCACCACCATCACTAATAGT
TAATTAAGTCA 3' (SEQ ID NO 2)

3'CCTCCGGACGTGCACTAGCTCCCGTCTGTGGTAGTGGTGGTAGTGATTATCAATTAATTG
5' (SEQ ID NO 95)

SEQ ID NO 3 (HCC19A)

ATGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTACTGTCTGTCTGACCAATTCOA
GCTTCCGCTTATGAGGTGCGCAACGTGTCCGGGATGTACCATGTACGAACGACTGCT
CCAACTCAAGCATTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT
GCCCTGCGTTCGGGAGAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTC
GCAGCTAGGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCG
TTGGGGCGGCTGCTCTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTC
CTCGTCTCCAGCTGTTACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCA
ATTGCTCAATCTATCCCGGCCACATAACAGGTCACCGTATGGCTTGGGATATGATGAT
GAACTGGTGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCT
GTCGTGGACATGGTGGCGGGGGCCCATTTGGGGAGTCCTGGCGGGCCTCGCCTACTATT
CCATGGTGGGGAAGTGGGCTAAGGTTTTGATTGTGATGCTACTCTTTGCTCTCTAATAG

SEQ ID NO 5 (HCC110A)

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TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTG

Fig. 21B

TTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCA
CCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG
CCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACG
GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGG
GGGCCCCATTGGGGAGTCCTGGCGGGTCTCGCCTACTATTCCATGGTGGGGAACCTGGGC
TAAGGTTTTGATTGTGATGCTACTCTTTGCTCCCTAATAG

SEQ ID NO 7 (HCC111A)

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TTCCGCTCGTCSGGCGCCCCCTAGGGGGTGTGCCAGAGCCCTGGCGCATGGCGTCCG
GGTTCTGGAAGACGGCGTGAACATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTA
TCTTCCTCTTGGCTTTACTGTCTGTCTGACCATTCCAGCTTCGGCTTATGAGGTGCCG
AACGTGTCCGGGATGTACCATGTCAACGAACGACTGCTCCAACCTCAAGCATTGTGTATG
AGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTCGGGAGAACCA
ACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGT
CCCCACTACGACAATACGACGCCACGTGCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTT
CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTACCC
ATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCC
ACATAACAGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 9 (HCC112A)

ATGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCCCTGCTGTCTGTCTGACCATACCA
GCTTCCGCTTATGAAGTGCAGAACGTGTCCGGGGTGTACCATGTCAACGAACGACTGCT
CCAACCTCAAGCATAGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT
GCCCTGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCACGCTC
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTGCGATTTGCTC
GTTGGGGCTGCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTT
CCTTGTTTCCCAGCTGTTACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCCGGCCATGTATCAGGTCAACGCATGGCTTGGGATATGATGAT
GAACTGGTCCTAATAG

SEQ ID NO 11 (HCC113A)

ATGTCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCCCTGCTGTCTGTCTGACCATACCA
GCTTCCGCTTATGAAGTGCAGAACGTGTCCGGGGTGTACCATGTCAACGAACGACTGCT
CCAACCTCAAGCATAGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT

Fig. 21C

GCCCTGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTC
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTTCGATTTGCTC
GTTGGGGCTGCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTT
CCTTGTTTCCAGCTGTTACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAT
GAACTGGTAATAG

SEQ ID NO 13 (HCC117A)

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TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAAGACGGCGTGAACATGCAACAGGGAAATTTGCCTGGTTGCTCTTTCTCTA
TCTTCCTCTTGGCTTTACTGTCTGTCTAACCATTCCAGCTTCCGCTTACGAGGTGCGC
AACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTATG
AGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCCGGGAGAACA
ACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCGGCTAGGAACGCCAGCAT
CCCCACTACAACAATACGACGCCACGTTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTT
CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCTCGTCTCCAGCTGTTACCC
ATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCC
ACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTACTAATAG

SEQ ID NO 15 (HCP51)

ATGCCCGGTTGCTCTTTCTCTATCTT

SEQ ID NO 16 (HCP52)

ATGTTGGGTAAAGGTCATCGATACCCT

SEQ ID NO 17 (HCP53)

CTATTAGGACCAGTTCATCATCATATCCCA

SEQ ID NO 18 (HCP54)

CTATTACCAGTTCATCATCATATCCCA

SEQ ID NO 19 (HCP107)

ATACGACGCCACGTTCGATTTCCAGCTGTTCAACATC

Fig. 21D

SEQ ID NO 20 (HCP108)

GATGGTGAACAGCTGGGAATCGACGTGGCGTCGTAT

SEQ ID NO 21 (HCC137)

ATGTTGGGTAAGGTCATCGATACCCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGATTCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTCCCTACAACGGCCCTGGTGGTAT
CGCAGCTGCTCCGATCCACAAAGCTGTCTGTGGACATGGTGGCGGGGGCCCAATTGGGG
AGTCCTGGCGGGTCTCGCTACTATTCCATGGTGGGGAACGGGCTAAGGTTTTGATTG
TGATGCTACTCTTTGCTCCCTAATAG

SEQ ID NO 23 (HCC138)

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TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACCTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGATTCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTAA
TAG

SEQ ID NO 25 (HCC139)

ATGTTGGGTAAGGTCATCGATACCCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT

Fig. 21E

ATCTTCCTCTTGGCTTTGCTGTCTGTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGATTCCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTGCCTACAACGGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCCTCTAATAG

SEQ ID NO 27 (HCCI40)

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TTCCGCTCGTCCGGCSCCCSCCTAGGGGGCCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTCTGAGGACGGCGTGAACATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT
ATCTTCCTCTTGGCTTTGCTGTCTGTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTACGAACGACTGCTCCAACTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTGATTCCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTGCCTACAACGGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCCTGATCGAGGGCAGACACCATCACCACCATCACTAATAG

SEQ ID NO 29 (HCCI62)

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CGCTCGTCCGGCCTCCCGTAGGAGGCGTCGCAAGAGCCCTTGCGCATGGCGTGAGGGC
CCTTGAAGACGGGATAAAATTCGCAACAGGGAATTTGCCCGGTTGCTCCTTTCTATTT
TCCTTCTCGCTCTGTTCTCTTGCTTAATTCATCCAGCAGCTAGTCTAGAGTGGCGGAAT
ACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGC
CGATGACGTTATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGGCAATACA
TCCACGTGCTGGACCCAGTGACACCTACAGTGGCAGTCAAGTACGTCCGAGCAACCA
CCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGATGTGCTCTGC
GCTCTACGTGGGTGACATGTGTGGGGCTGTCTTCCTCGTGGGACAAGCCTTCACGTTCA
GACCTCGTCCCATCAAACGGTCCAGACCTGTAACCTGCTCGCTGTACCCAGGCCATCT
TTCAGGACATCGAATGGCTTGGGATATGATGATGAACTGGTAATAG

Fig. 21F

SEQ ID NO 31 (HCC163)

ATGGGTAAGGTCATCGATACCCTAACGTGCGGATTGCGCCATCTCATGGGGTATATCC
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CCTTGAGGACGGGGTAAACTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCT
TTATTCTTGCTCTTCTCTCTGTCTGACCGTTCCGGCCTCTGCAGTTCCCTACCGAAATG
CCTCTGGGATTTATCATGTTACCAATGATTGCCCAAACCTCTTCCATAGTCTATGAGGCA
GATAACCTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTCATGACAGGTAATGTGA
GTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCAC
GGCTCCTCTTCGGAGAGCCGTTGACTACCTAGCGGGAGGGGCTGCCCTCTGCTCCGCG
TTATACGTAGGAGACGCGTGTGGGGCACTATTCTTGGTAGGCCAAATGTTACCTATA
GGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGCCATGT
TACCGGCCACCGGATGGCATGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 33 (HCP109)

TGGGATATGATGATGAACTGGTC

SEQ ID NO 34 (HCP72)

CTATTATGGTGGTAAKGCCARCARGAGCAGGAG

SEQ ID NO 35 (HCC122A)

TGGGATATGATGATGAACTGGTCGCTACAACGGCCCTGGTGGTATCGCAGCTGCTCC
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GCCTCGCCTACTATTCCATGGTGGGGAACCTGGGCTAAGGTTTTGGTTGTGATGCTACTC
TTTGCCGGCCTCGACGGGCATACCCGCGTGTGAGGAGGGGCGAGCAGCCTCCGATACCA
GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTGCGGCTCAGAAAATCCAGCTCGTAAACAC
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAAC
AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAG
CGCTTGGCCAGCTGTCTCTCATCGACAAGTTGCTCAGGGGTGGGGTCCCCTCACTT
ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC
GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGATTGCTTACCCCCGAGCC
CTGTTGTGGTGGGGACGACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAA
CGACTCGGATGTGCTGATTCTCAACAACACGCGGGCCGCGAGGCAACTGGTTCGGC
TGTACATGGATGAATGGCACTGGGTTTACCAAGACGTGTGGGGGGCCCCCGTGAACA
TCGGGGGGGGCCGGCAACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCC
CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT

Fig. 21G

CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCTGAAGCCGCATGCAATTGGACTCG
AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCCGCTGCTGCTG
TCTACAACAGAGTGGCAGATACTGCCCTGTTCTTCACCACCCTGCCGGCCCTATCCA
CCGGCCTGATCCACCTCCATCAGAACATCGTGGACGTGCAATACCTGTACGGTGTAGG
GTCGGCGGTTGTCTCCCTTGTCATCAAATGGGAGTATGTCCTGTTGCTCTTCTTCTCCT
GGCAGACGCGCGCATCTGCGCCTGCTTATGGATGATGCTGCTGATAGCTCAAGCTGAG
GCCGCCCTTAGAGAACTGGTGGTCTCAATGCCGGCGCCGTGGCCGGGGCGCATGGC
ACTCTTTCTTCTTCTTGTGTTCTTCTGTGCTGCCTGGTACATCAAGGGCAGGCTGGTCCC
TGGTGCGGCATACGCCCTTCTATGGCGTGTGGCCGCTGCTCCTGCTTCTGCTGGCCTTAC
CACCACGAGCTTATGCCTAGTAA

SEQ ID NO 37 (HCCI41)

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CCTCGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTTTGGTTGTGATGCTACTCT
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GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTGCGCTCAGAAAATCCAGCTCGTAAACAC
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAAC
AGGGTTCTTTGCCGCACTATTCTACAAACACAAAATTCAACTCGTCTGGATGCCCAGAG
CGCTTGGCCAGCTGTGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCCTCACTT
ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC
GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTACCCCCGAGCC
CTGTTGTGTTGGGGACGACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAA
CGACTCGGATGTGCTGATTCTCAACAACACGCGGCCCGCCGCGAGGCAACTGGTTCGGC
TGTACATGGATGAATGGCACTGGGTTCCACCAAGACGTGTGGGGGGCCCCCGTGCAACA
TCGGGGGGGGCCGGCAACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCC
CGAGGCCACCTACGCCAGATGCGGTTCTGGGGCCCTGGCTGACACCTAGGTGTATGGTT
CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCTGAAGCCGCATGCAATTGGACTCG
AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCCGCTGCTGCTG
TCTACAACAGAGTGGCAGAGTGGCAGAGCTTAATTAATTAG

SEQ ID NO 39 (HCCI42)

GATCCACACAAGCTGTGCTGGACATGGTGGCGGGGGCCCATTTGGGGAGTCCTGGCGGG
CCTCGCCTACTATTCCATGGTGGGGAAGTGGGCTAAGGTTTTGGTTGTGATGCTACTCT

Fig. 21H

TTGCCGGCGTCGACGGGCATACCCGCGTGTCTAGGAGGGGCAGCAGCCTCCGATACCA
GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTGGGCTCAGAAAATCCAGCTCGTAAACAC
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAAC
AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAG
CGCTTGGCCAGCTGTGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT
ACACTGAGCCTAACAGCTCGGACCAGAGGGCCCTACTGCTGGCACTACGCGCCTCGACC
GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC
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CGACTCGGATGTGCTGATTCTCAACAACACGCGCGCCGCCGAGGCAACTGGTTCGGC
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TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTGGAAGCCGCATGCAATTGGACTCG
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TCTACAACAGGTGATCGAGGGCAGACACCATCACCACCATCACTAATAG

SEQ ID NO 41 (HCC143)

ATGGTGGGGAACTGGGCTAAGGTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG
GGCATACCCGCGTGTCTAGGAGGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT
CTTTAGCCCCGGGTGGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC
ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC
TATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGTGCG
CTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGC
TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG
CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC
GACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTG
ATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG
GCACTGGGTTACCAAGACGTGTGGGGGCCCCCGTGCAACATCGGGGGGGCCGGCA
ACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC
CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG
CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG
GGGCGTGGAGCACAGGTTGGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA
CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGG
CAGAGCTTAATTAATTAG

Fig. 21I

SEQ ID NO 43 (HCC144)

ATGGTGGGGAAC TGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG
GGCATACCCGCGTGT CAGGAGGGGGCAGCAGCCTCCGATACCAGGGGCCCTTGTGTCCCT
CTTTAGCCCCGGGTGGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC
ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC
TATTCTACAAACACAAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCS
CTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCCTCACTTACACTGAGCCTAACAGC
TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG
CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC
GACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTG
ATTCTCAACAACACGCGGGCCGCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG
GCACTGGGTTACCAAGACGTGTGGGGGGCCCCCGTGCAACATCGGGGGGGCCGGCA
ACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC
CAGATGCGGTTCTGGGGCCCTGGCTGACACCTAGGTGTATGGTTCAATTACCCATATAGG
CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG
GGGCGTGGAGCACAGGTTCSAAGCCGCATGCAATTGGA CTGAGGAGAGCGTTGTGA
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SEQ ID NO 45 (HCC164)

ATGGTGGCGGGGGGCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGG
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GCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCAATTACCCATATAGGCTCTGG
CACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGGGGGCG

Fig. 21J

TGGAGCACAGGTTTGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGA
GGACAGGGATAGATCAGAGCTTAGCCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATA
CTGCCCTGTTCTTCACCACCCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCA
GAACATCGTGGACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTC
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CTGCTTATGGATGATGCTGCTGATAGCTCAAGCTGAGGGCCGCTTAGAGAACCTGGTG
GTCCTCAATGCGGCGGCCGTGGCCGGGGCGCATGGCACTCTTCTCTCTTGTGTTCTT
CTGTGCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCGGCATACGCCTTCTAT
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SEQ ID NO 47 (HCC165)

AATTTGGGTAAGGTCATCGATACCCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
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ATCTTCTCTTGGCTTTGCTGTCTGTCTGACCGTTCCAGCTTCGGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTCAAGAACGACTGCTCCAACCTCAAGCATTGTGTAT
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AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAAATACGACGCCACGTGATTTGCTCGTTGGGGCGGCTGCTTTCTG
TTCCGCTATGTACGTGGGGACCTCTGCGGATCTGTCTTCTCTCTCTCCAGCTGTTCA
CCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG
CCACATAACGGGTACCGTATGGCTTGGGATATGATGATGAACCTGGTGCCTACAACG
GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCAAGCTGTGCTGGACATGGTGGCGG
GGGCCCCATTGGGGAGTCTGGCGGGCCCTCGCCTACTATTCCATGGTGGGGAACTGGGC
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GAGGGGCAGCAGCCTCCGATACCAGGGGCCCTTGTGTCCCTCTTTAGCCCCGGGTGCGC
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CCAGTGTATTGCTTACCCCCGAGCCCTGTTGTGGTGGGGACGACCGATCGGTTTGGTGT
CCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAACACGCGG
CCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTACCAAGA
CGTGTGGGGGCCCCCGTGCAACATCGGGGGGGCCGGCAACAACACCTTGACCTGCC

Fig. 21K

CCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTCTGGGCC
CTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTACCCCTGCA
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CGAAGCCGCATGCAATTGGA CTGAGGAGAGCGTTGTGACTTGGAGGACAGGGATAG
ATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCCCTGTTCC
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TGATGCTGCTGATAGCTCAAGCTGAGGCCCGCTTAGAGAACCTGGTGGTCTCAATGC
GGCGGCGCTGGCCGGGGCGCATGGCACTCTTCTCTCTGTTCTCTGTGCTGCCT
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GCTGCTCCTGCTTCTGCTGGCCTTACCACCACGAGCTTATGCCTAGTAAGCTT

SEQ ID NO 49 (HCC168)

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CTCGTGGGAGGCGACAACCTATCCCCAAGGCTCGCCGACCCGAGGGTAGGGCCTGGG
CTCAGCCCGGGTACCCTTGGCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATG
GCTCCTGTCACCCCGCGGCTCTCGGCCTAGTTGGGGCCCTACAGACCCCGCGGTAGG
TCGCGTAATTTGGGTAAGGTCATCGATACCCTTACATGCGGGCTTCGCGACCTCGTGG
GGTACATTCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGG
CGTCCGGGTTCTGGAGGACGGCGTGAACATGCAACAGGGAAATTTGCCCGGTTGCTCT
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GTGCGCAACGTGTCCGGGATGTACCATGTGACGAACGACTGCTCCAACCTCAAGCATTG
TGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTCGGGA
GAACAACCTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCC
AGCGTCCCCACACGACAATACGACGCCACGTGATTTGCTCGTTGGGGCGGCTGCTT
TCTGTTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCTCGTCTCCAGCTG
TTCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATC
CCGGCCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTGCCTAC
AACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCACAAAGCTGTCGTGGACATGGTG
GCGGGGGCCCCATTGGGGAGTCTGGCGGGCCTCGCCTACTATTCATGGTGGGGAACT
GGGCTAAGGTTTTGGTTGTGATGCTACTCTTGGCGGCGTCGACGGGCATACCCGCGT
GTCAGGAGGGGCAGCAGCCTCGATACCAGGGGCCTTGTGTCCCTCTTACCCCCGGG

Fig. 21L

TCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACT
GCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCACTATTCTACAAAC
ACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGTGCTCCATCGACAA
GTTGCTCAGGGGTGGGGTCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGG
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GCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGACGACCGATCGGTT
TGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAAC
ACGCGGCCCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTCA
CCAAGACGTGTGGGGGGCCCCCGTGCAACATCGGGGGGGCCGGCAACAACACCTTGA
CCTGCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTG
TGGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTAC
CCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGGGGGCGTGGAGC
ACAGGTTGGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACA
GGGATAGATCAGAGCTTAGCCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCC
CTGTTCCCTTCAACACCCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCAGAAC
ATCGTGGACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTATCA
AATGGGAGTATGTCCTGTTGCTCTTCTCTCTGCGCAGACGCGCGCATCTGCGCCTGC
TTATGGATGATGCTGCTGATAGCTCAAGCTGAGGCCGCCCTTAGAGAACCTGGTGGTCC
TCAATGCCGGCGCCGTGGCCGGGGCGCATGGCACTCTTTCCTTCTTGTGTTCTTCTGT
GCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGGGCCATACGCCCTTCTATGGCG
TGTGGCCGCTGCTCCTGCTTCTGCTGGCCTTACCACCACGAGCTTATGCCTAGTAA

Fig. 22

		OD measured at 450 nm construct			
Fraction	volume dilution	39 Type 1b	40 Type 1b	62 Type 3a	63 Type 3a
START	23 ml 1/20	2.517	1.954	1.426	1.142
FLOW THROUGH	23 ml 1/20	0.087	0.085	0.176	0.120
1	0.4 ml 1/200	0.102	0.051	0.048	0.050
2		0.396	0.550	0.090	0.067
3		2.627	2.603	2.481	2.372
4		3	2.967	3	2.694
5		3	2.810	2.640	2.154
6		2.694	2.499	1.359	1.561
7		2.408	2.481	0.347	1.390
8		2.176	1.970	1.624	0.865
9		1.461	1.422	0.887	0.604
10		1.236	0.926	0.543	0.519
11		0.981	0.781	0.294	0.294
12		0.812	0.650	0.249	0.199
13		0.373	0.432	0.239	0.209
14		0.653	0.371	0.145	0.184
15		0.441	0.548	0.151	0.151
16		0.321	0.374	0.098	0.106
17		0.525	0.186	0.099	0.108
18		0.351	0.171	0.083	0.090
19		0.192	0.164	0.084	0.087

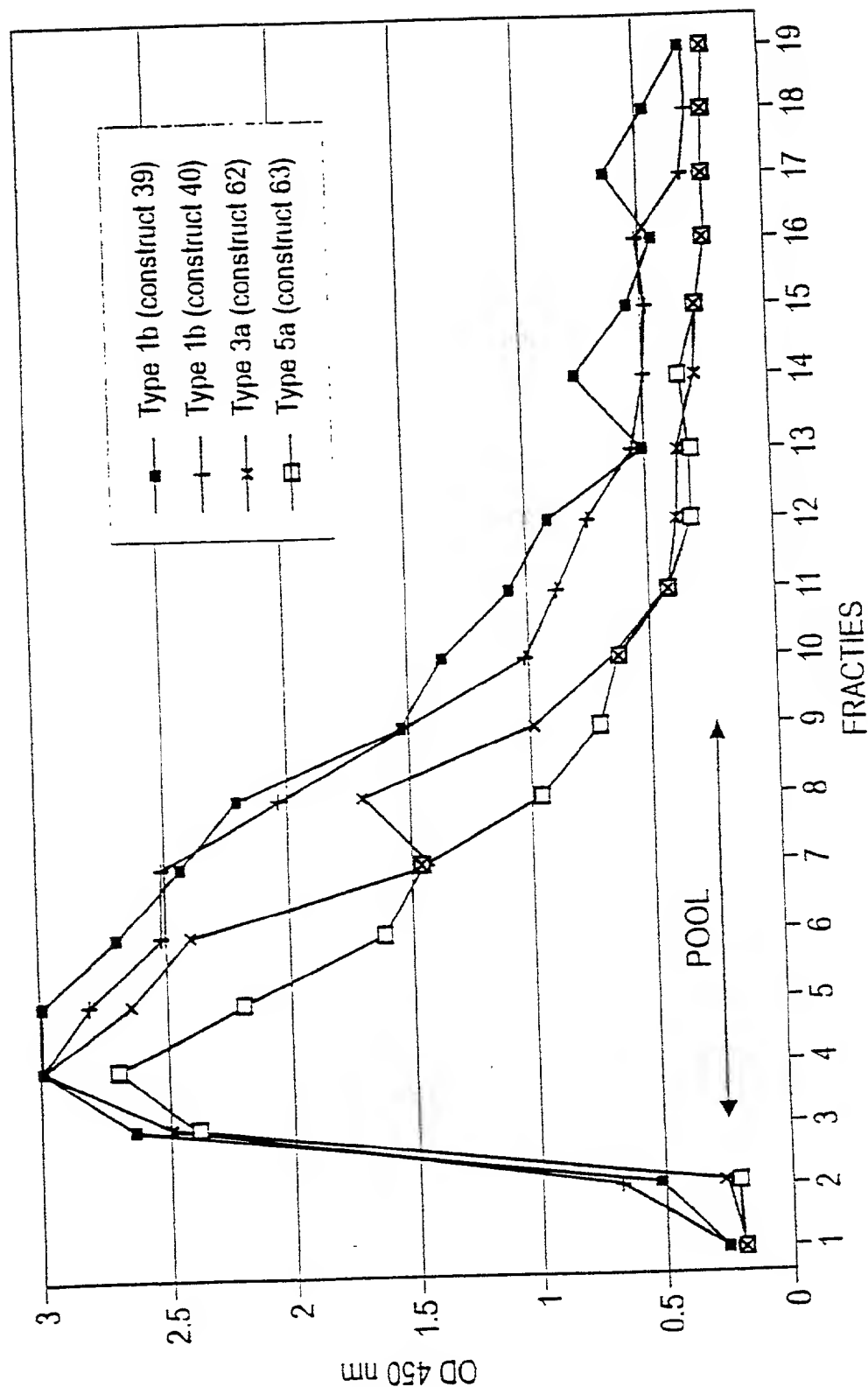


Fig. 23

Figure 24

Fraction	volume	dilution	OD measured at 450 nm			
			construct			
			39 Type 1b	40 Type 1b	62 Type 3a	63 Type 5a
20	250 μ l	1/200	0.072	0.130	0.096	0.051
21			0.109	0.293	0.084	0.052
22			0.279	0.249	0.172	0.052
23			0.093	0.151	0.297	0.054
24			0.080	0.266	0.438	0.056
25			0.251	0.100	0.457	0.048
26			3	1.649	0.722	0.066
27			3	3	2.526	0.889
28			3	3	3	2.345
29			3	3	2.849	2.580
30			2.227	1.921	1.424	1.333
31			0.263	0.415	0.356	0.162
32			0.071	0.172	0.154	0.064
33			0.103	0.054	0.096	0.057
34			0.045	0.045	0.044	0.051
35			0.043	0.047	0.045	0.046
36			0.045	0.045	0.049	0.040
37			0.045	0.047	0.046	0.048
38			0.046	0.048	0.047	0.057
39			0.045	0.048	0.050	0.057
40			0.046	0.049	0.048	0.049

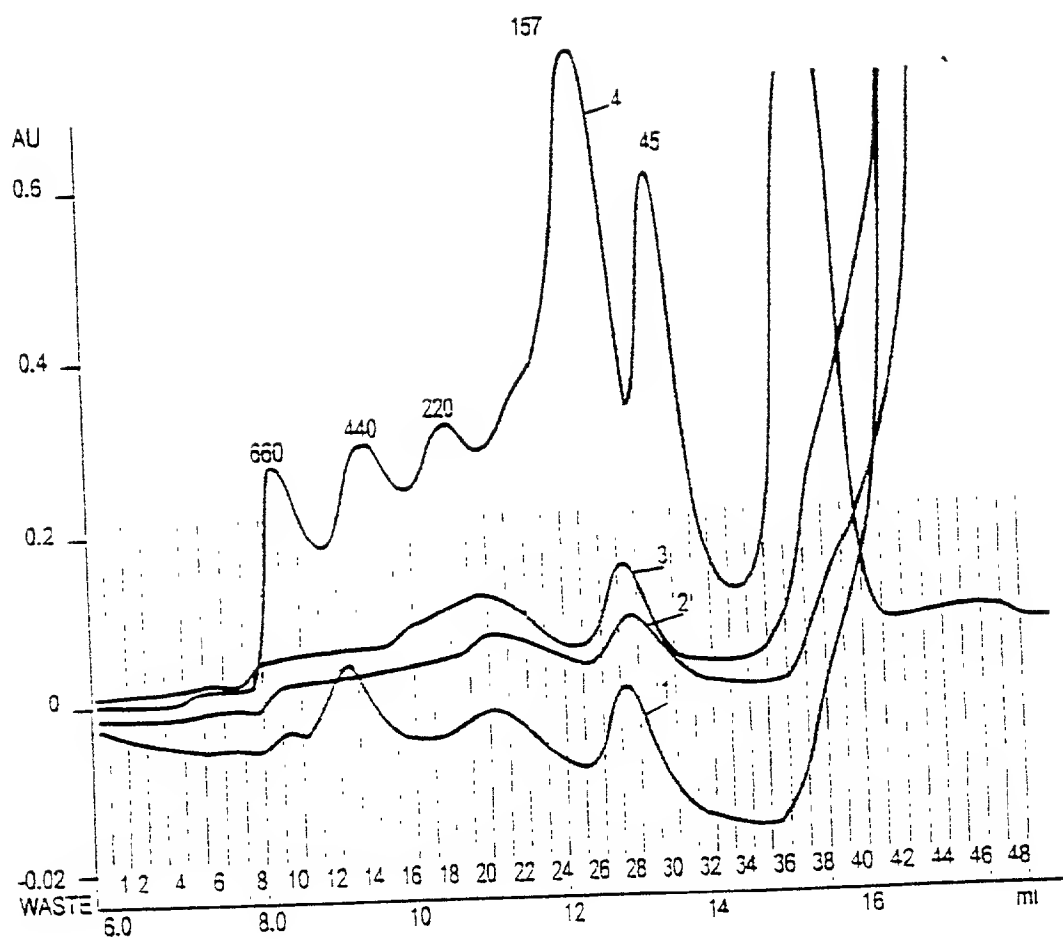


Fig. 25

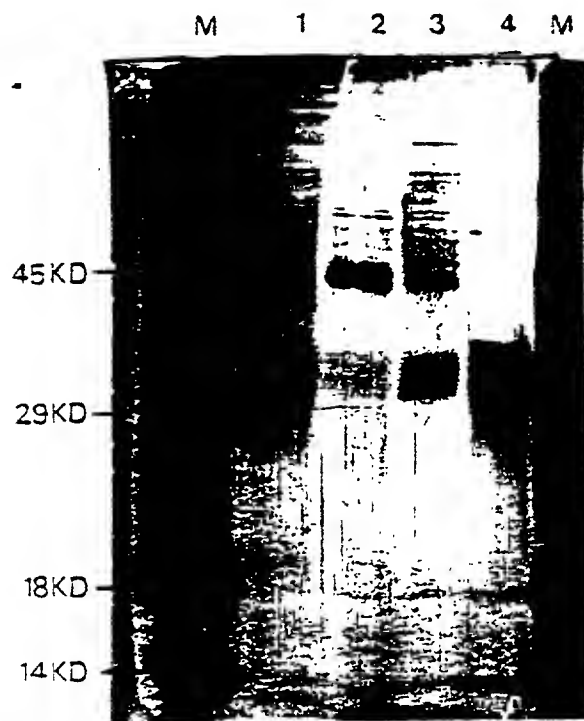


Fig. 26

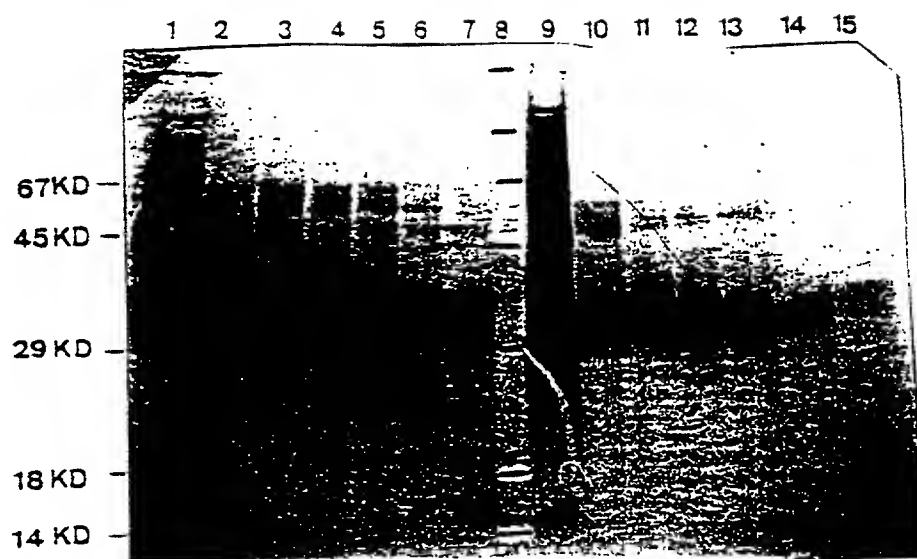


Fig. 27

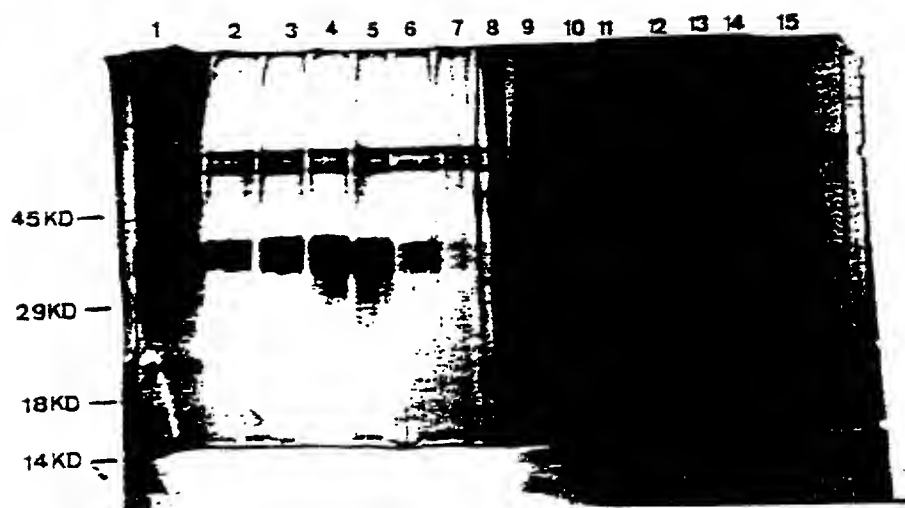


Fig.28

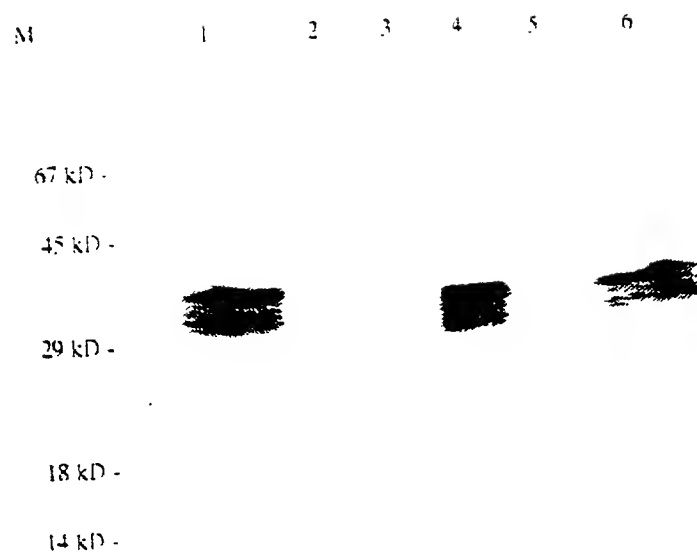


Fig.29

Lane 1: Crude Lysate
 Lane 2: Flow through Lentil Chromatography
 Lane 3: Wash with EMPIGEN Lentil Chromatography
 Lane 4: Eluate Lentil Chromatography
 Lane 5: Flow through during concentration lentil eluate
 Lane 6: Pool of E1 after Size Exclusion Chromatography

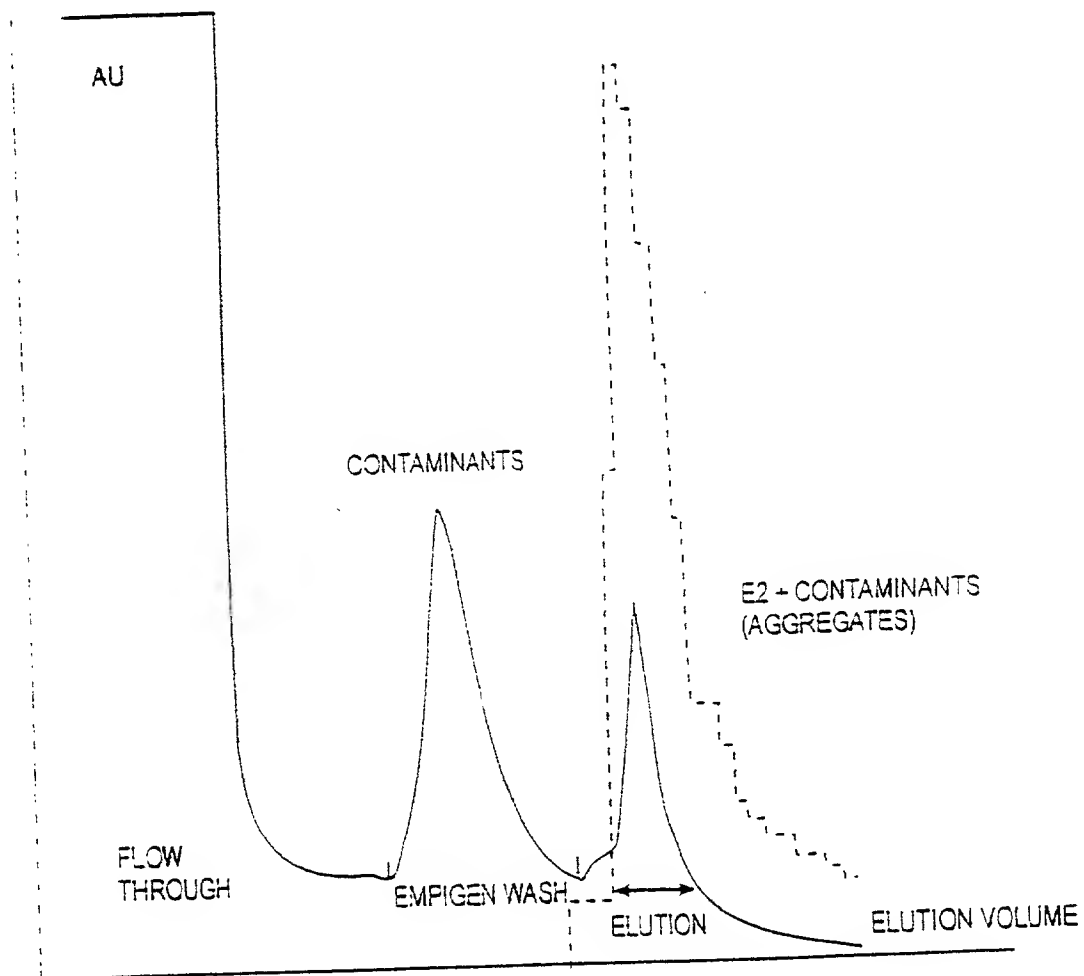
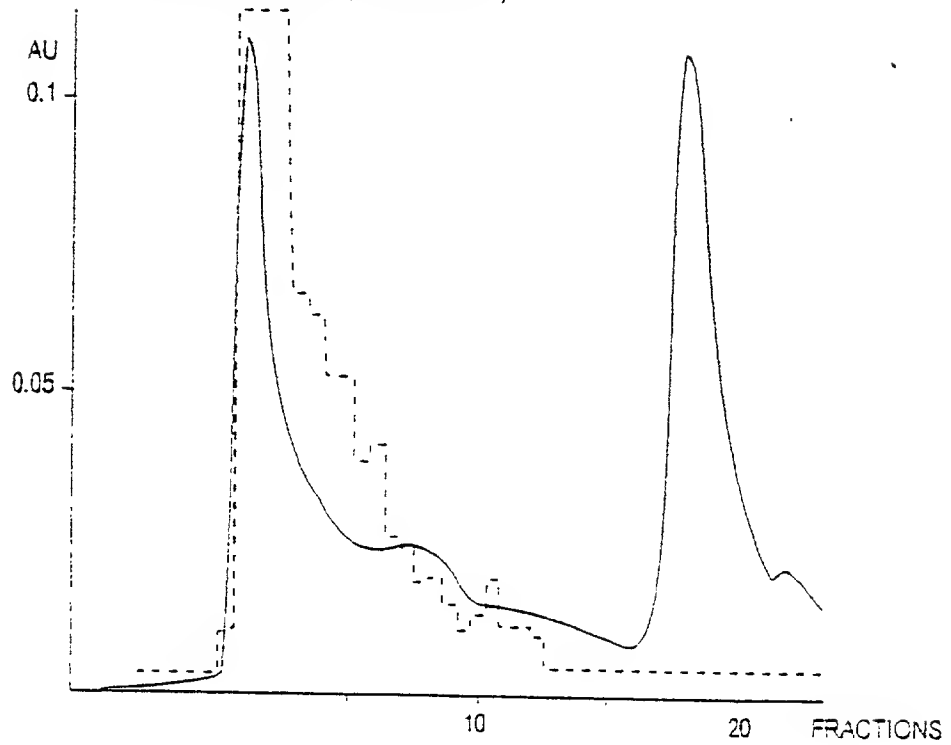


Fig. 30

NON-REDUCED

Fig. 31A

E2 + CONTAMINANTS (AGGREGATES)



REDUCED

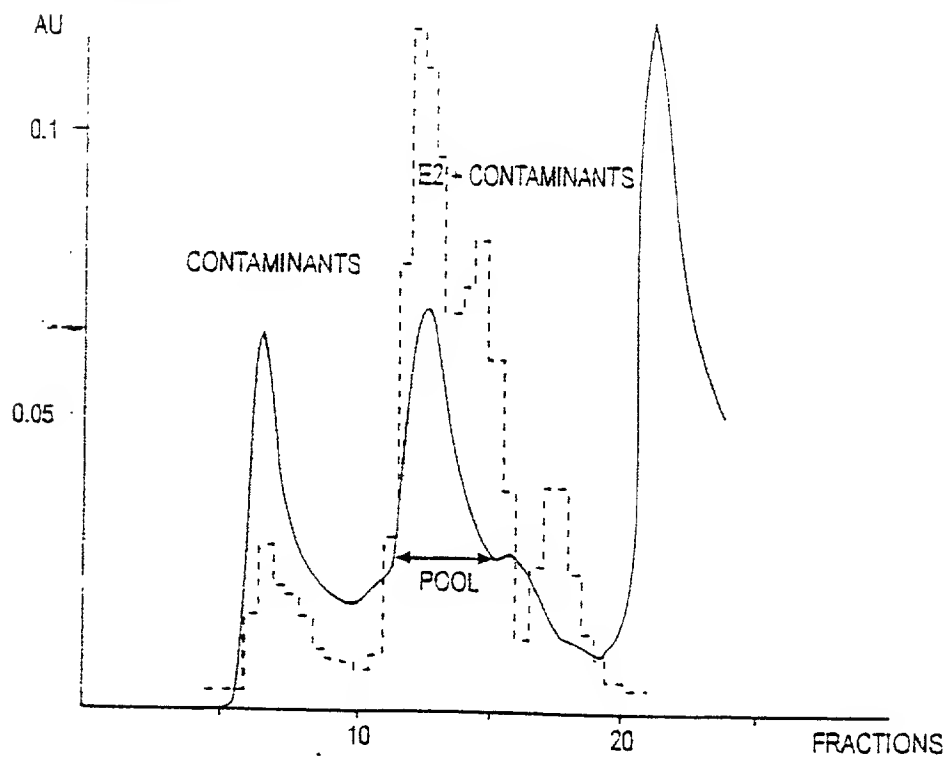


Fig. 31B

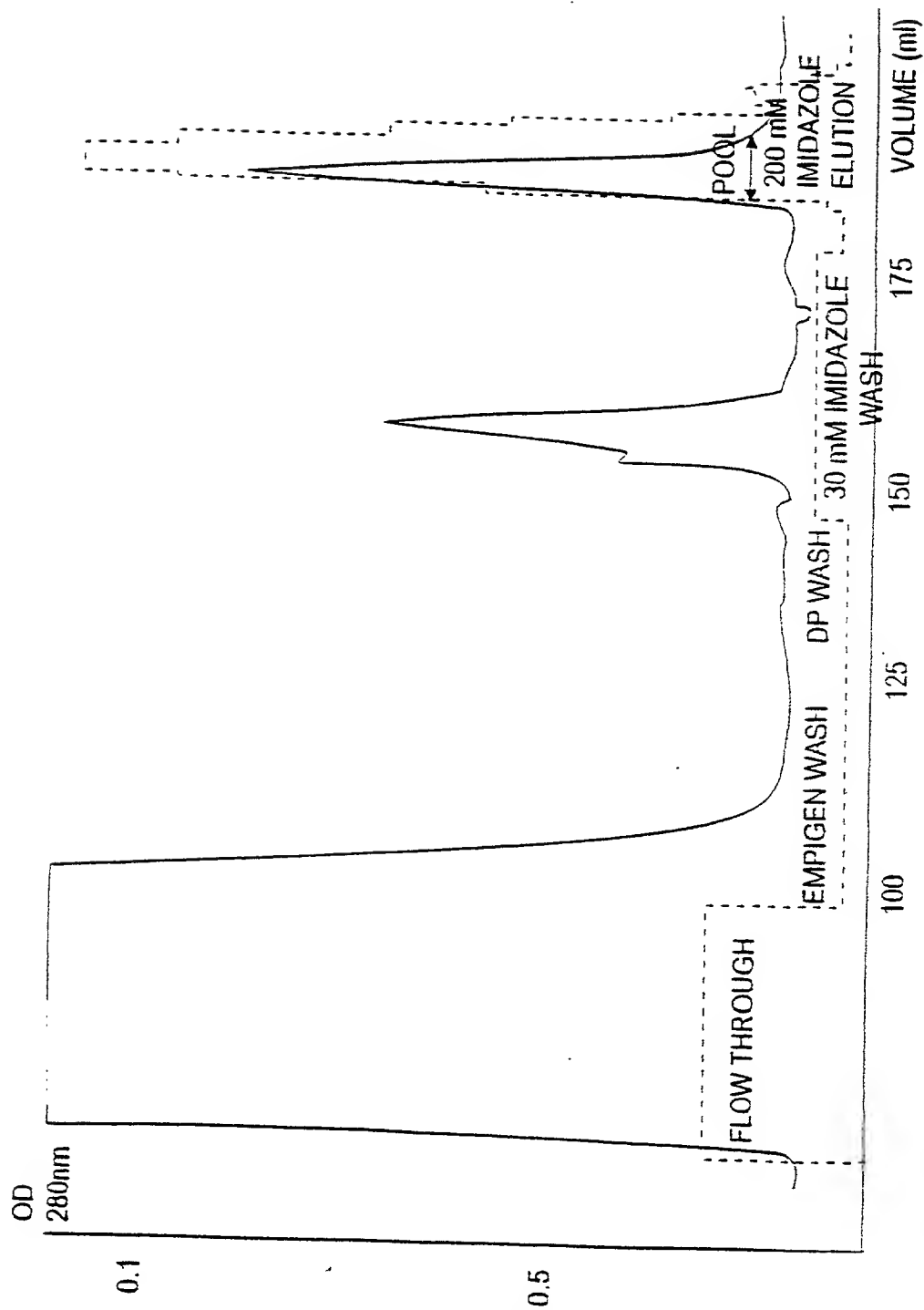
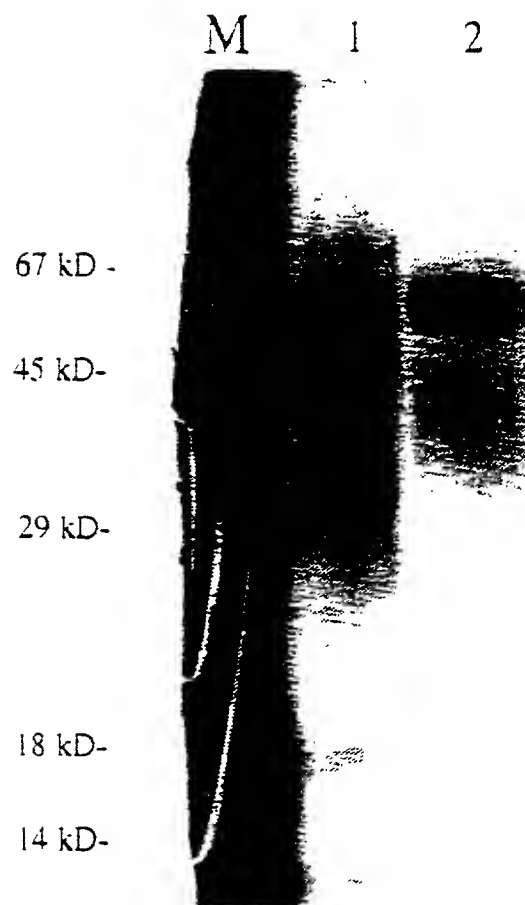


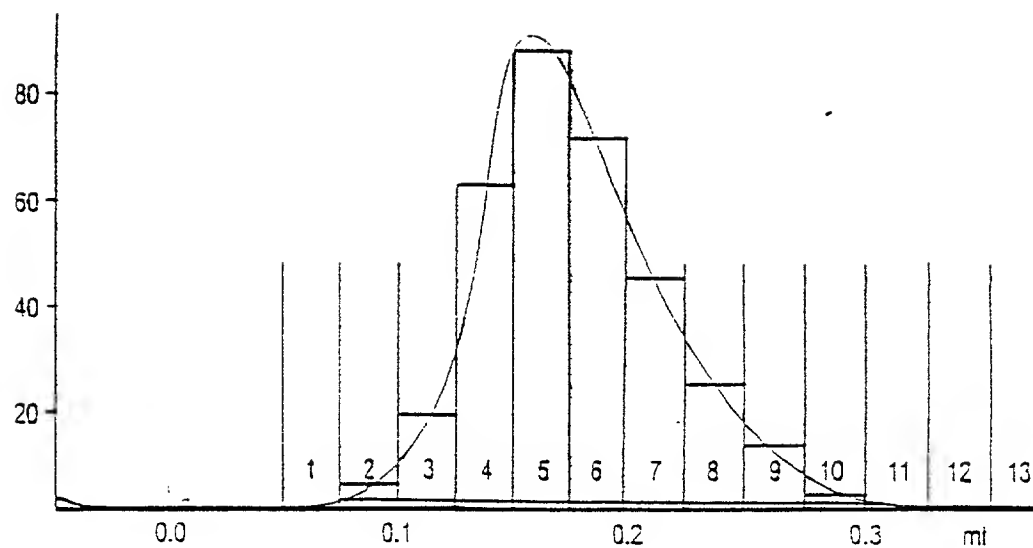
Fig. 32

SILVER STAIN OF PURIFIED E2



1. 30 mM IMIDAZOLE WASH Ni-IMAC
2. 0.5 μ g E2

Fig.33



No.	Ret. (mi)	Peak start (mi)	Peak end (mi)	Dur (mi)	Area (mi*mAU)	Height (mAU)
1	-0.45	-0.46	-0.43	0.04	0.0976	4.579
2	1.55	0.15	3.26	2.51	796.4167	889.377
3	3.27	3.26	3.31	0.05	0.0067	0.224
4	3.35	3.32	3.35	0.02	0.0002	0.018

Total number of detected peaks = 4
 Total Area above baseline = 0.796322 mi*AU
 Total area in evaluated peaks = 0.796321 mi*AU
 Ratio peak area / total area = 0.999999
 Total peak duration = 2.613583 mi

Fig. 34

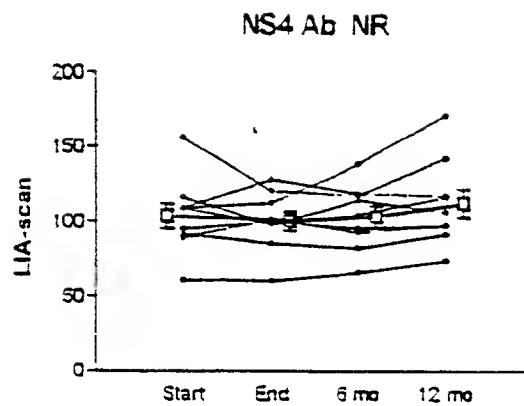


Fig. 35A-1

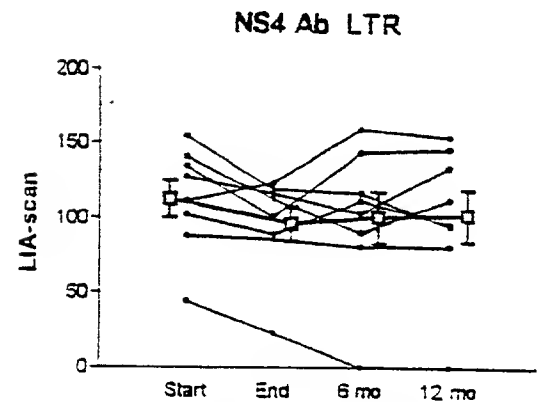


Fig. 35A-2

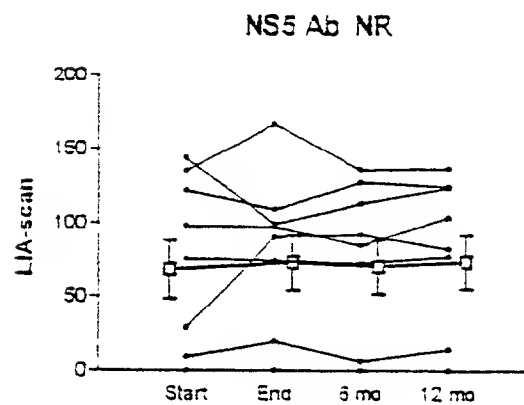


Fig. 35A-3

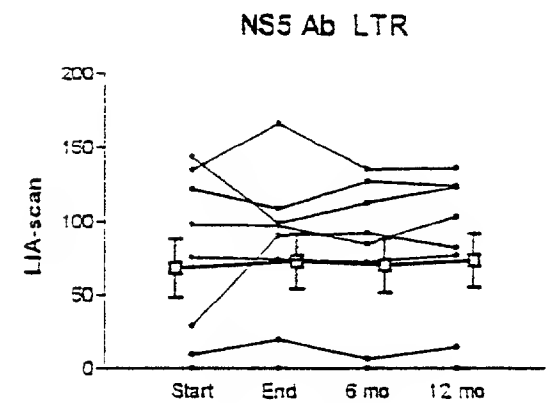


Fig. 35A-4

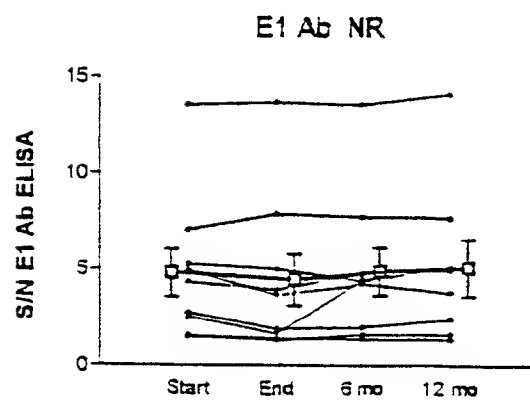


Fig. 35A-5

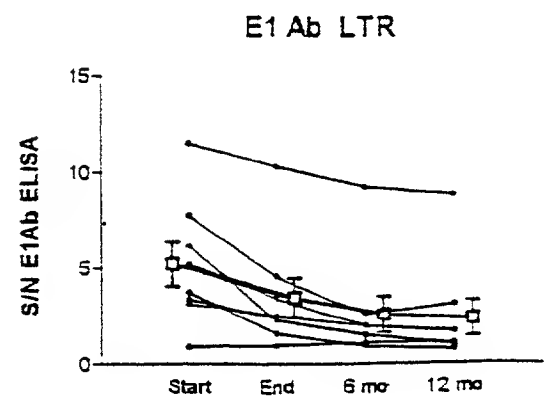


Fig. 35A-6

E2 Ab NR

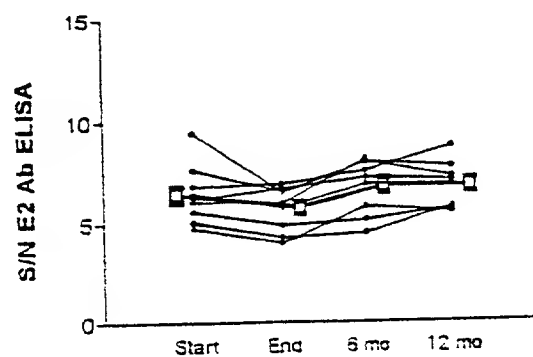


Fig. 35A-7

E2 Ab LTR

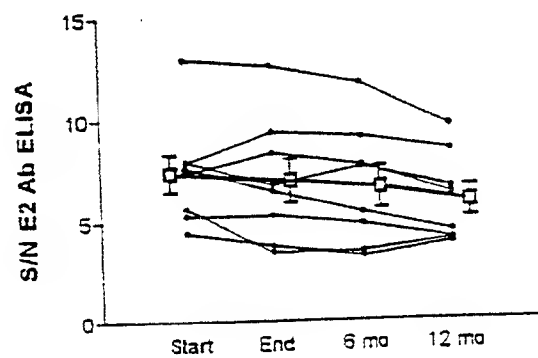


Fig. 35A-8

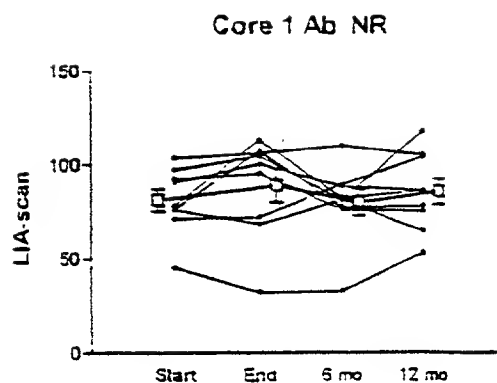


Fig. 35B-1

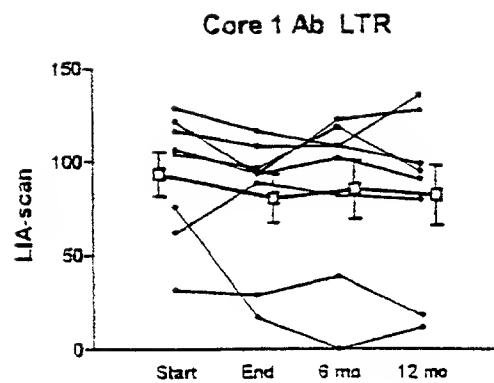


Fig. 35B-2

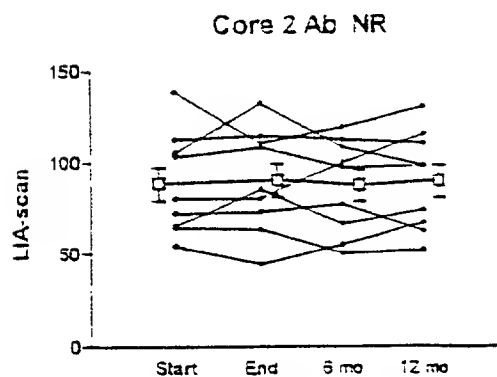


Fig. 35B-3

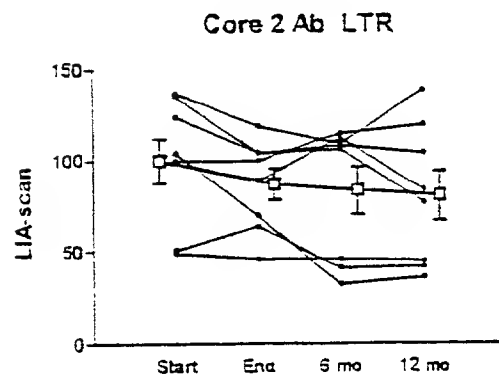


Fig. 35B-4

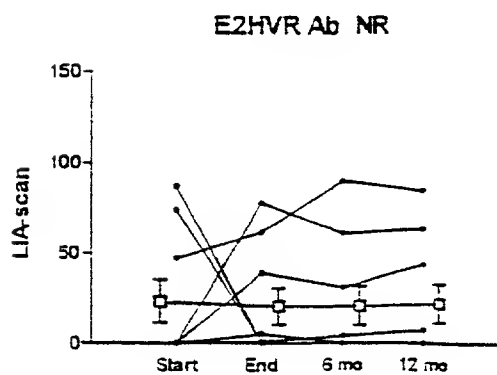


Fig. 35B-5

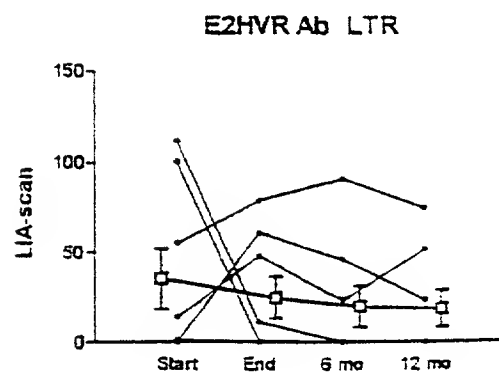


Fig. 35B-6

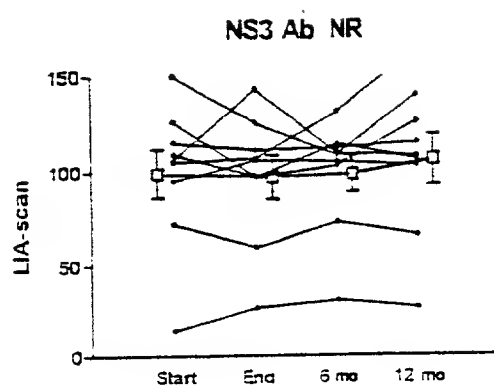


Fig. 35B-7

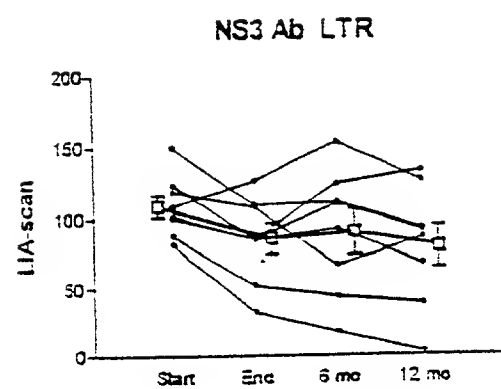


Fig. 35B-8

Fig. 36A

E1 Ab

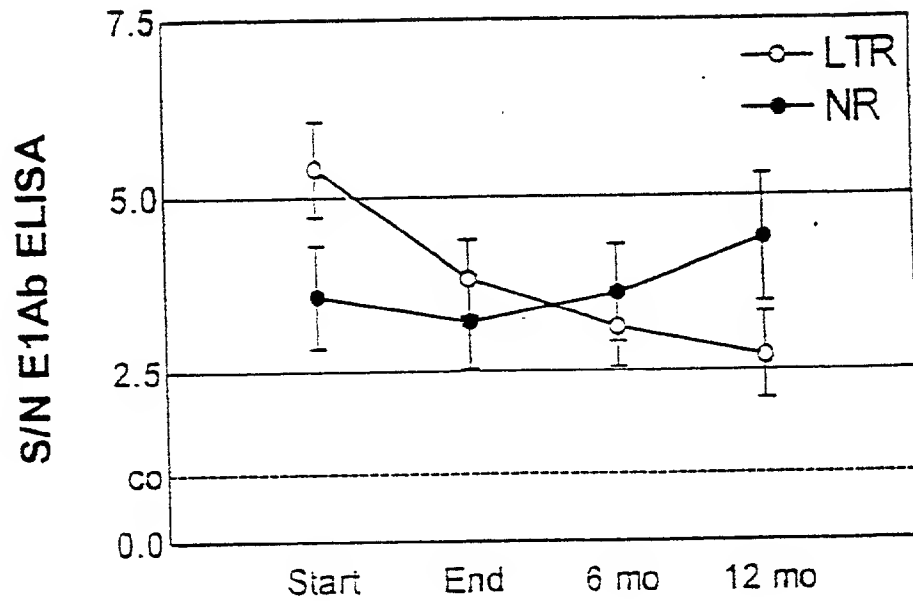


Fig. 36B

E2 Ab

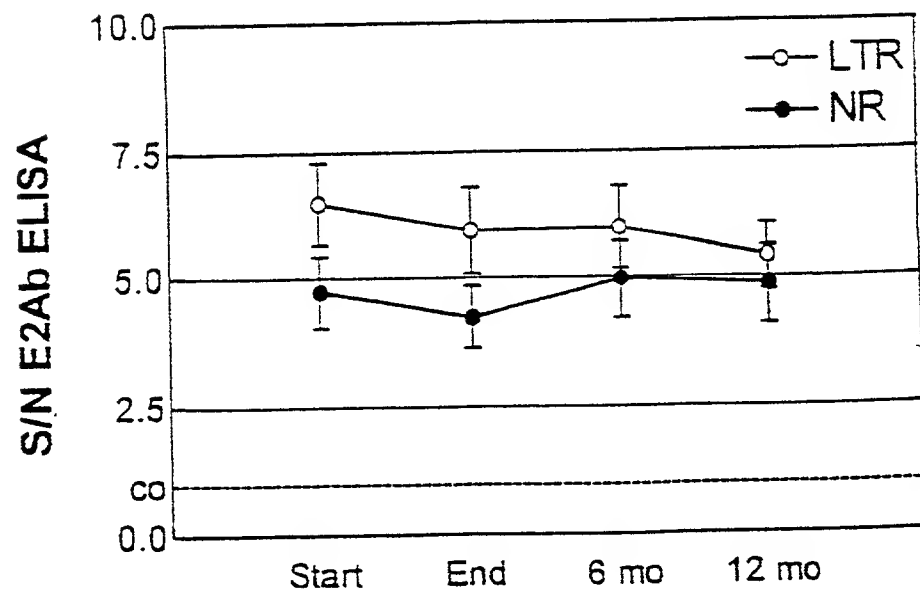


Fig. 37A
Non Responders

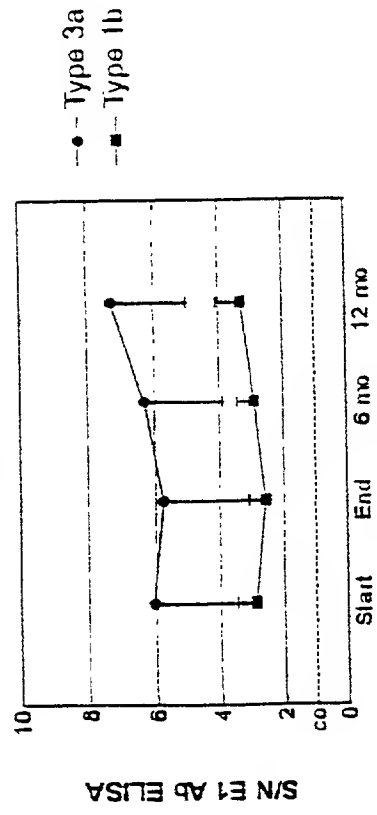


Fig. 37B
Long Term Responders

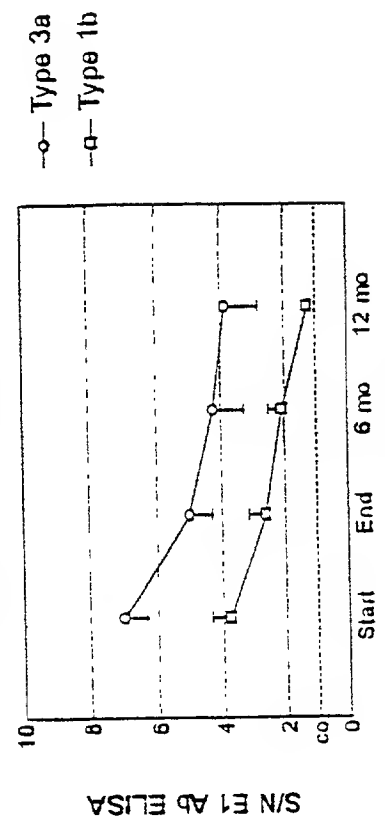


Fig. 37C
Type 1b

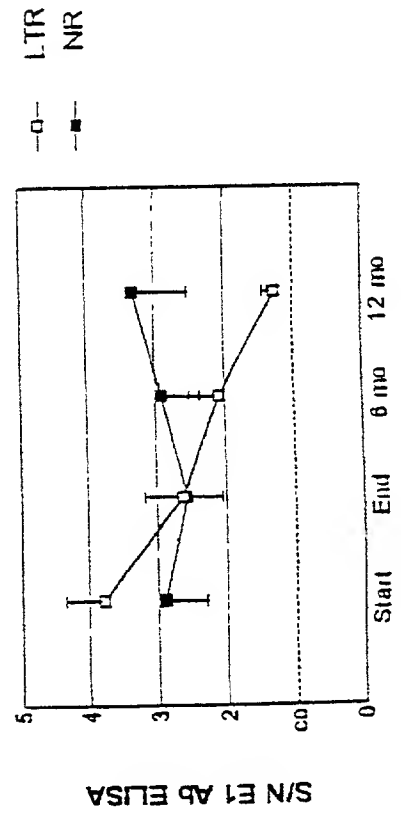


Fig. 37D
Type 3a

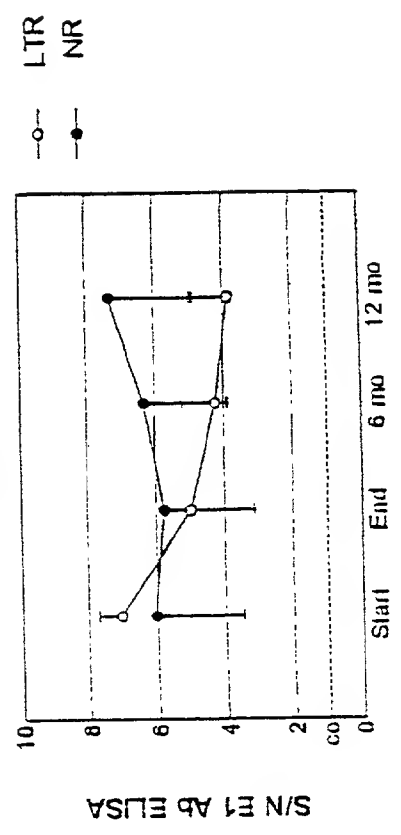


Fig. 38

Relative Map Positions of
anti-E2 monoclonal antibodies

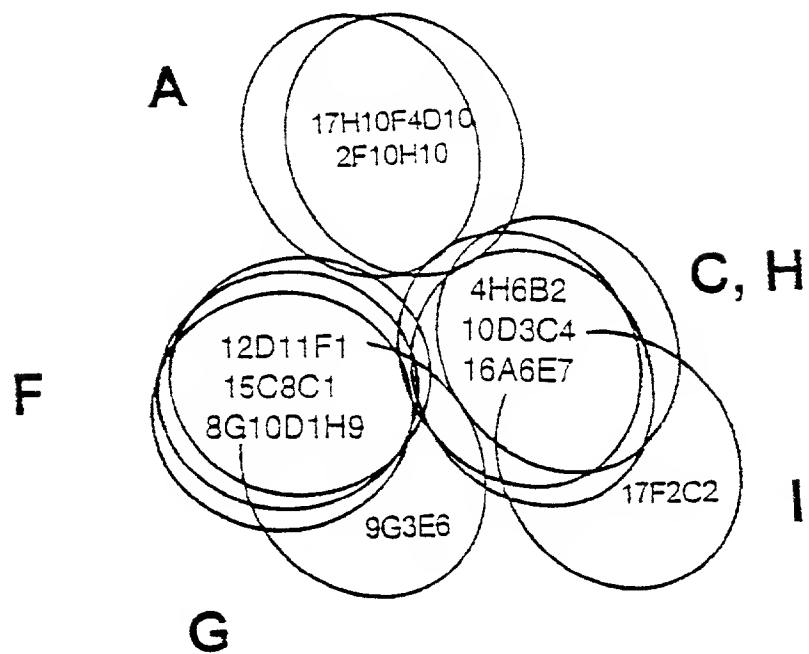
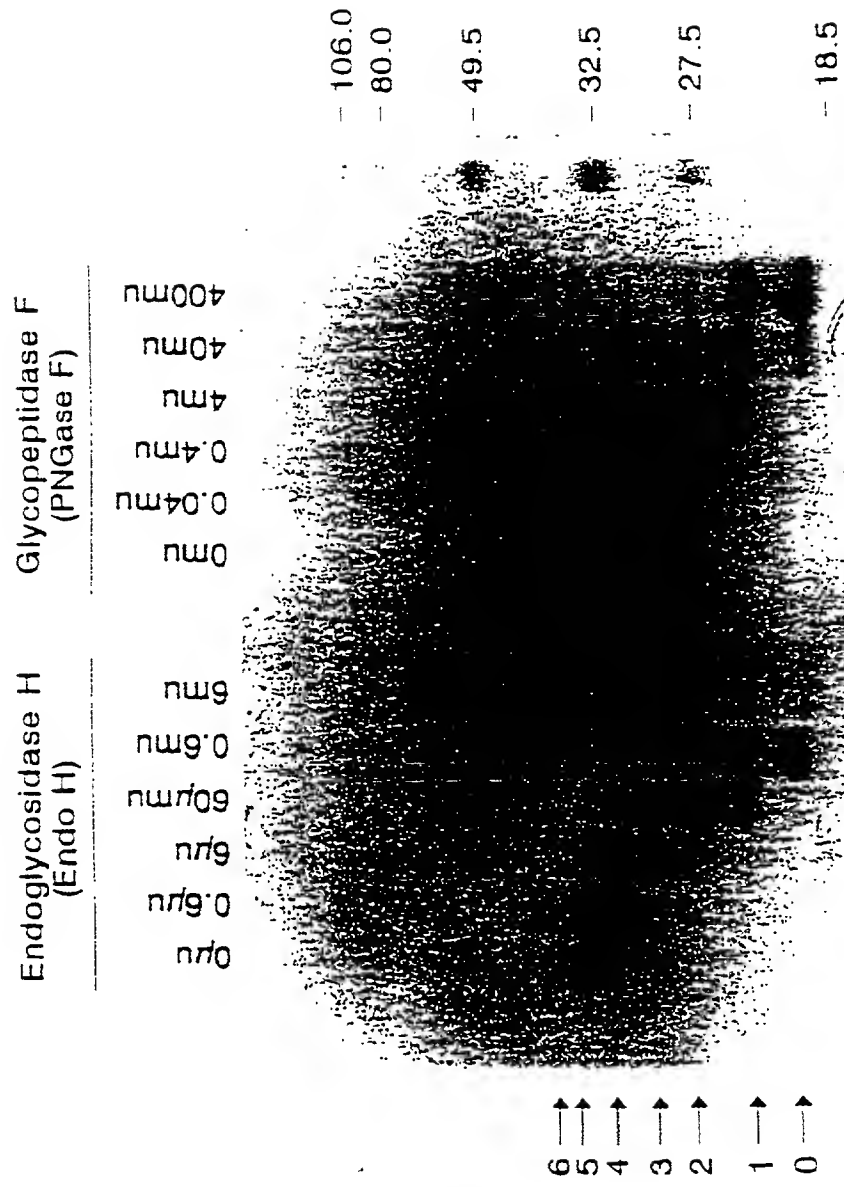


Fig.39

PARTIAL DEGLYCOSYLATION OF HCV E1 ENVELOPE PROTEIN



PARTIAL TREATMENT OF HCV E2/E2s ENVELOPE PROTEINS BY PNGase F

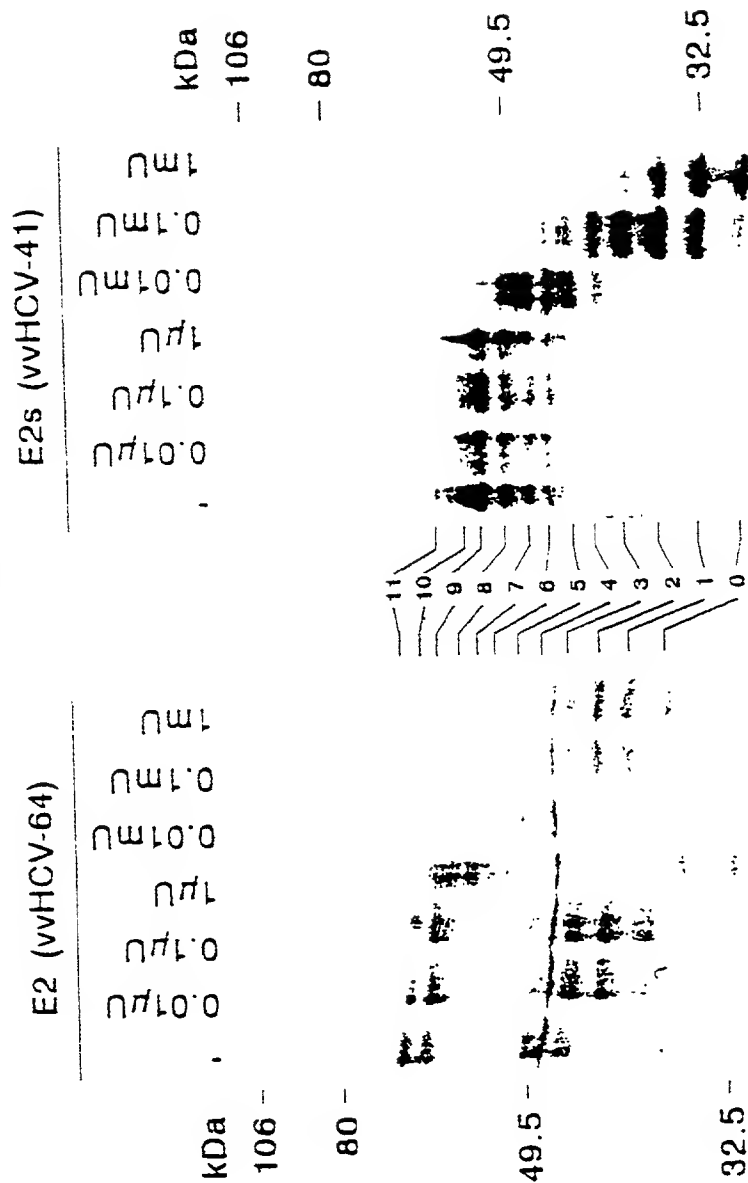


Fig. 40

Fig. 41 *In Vitro* Mutagenesis of HCV E1 glycoprotein

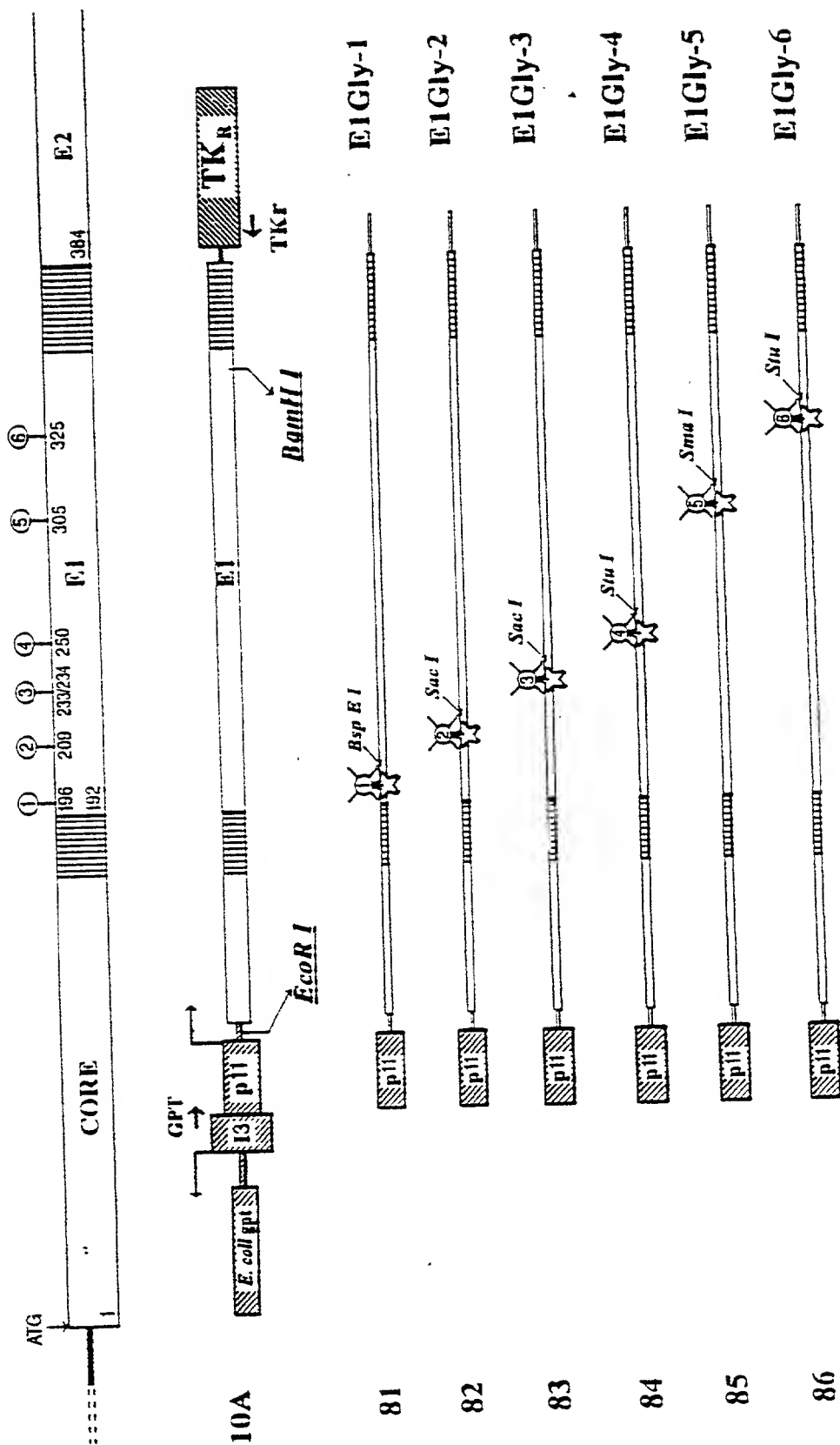
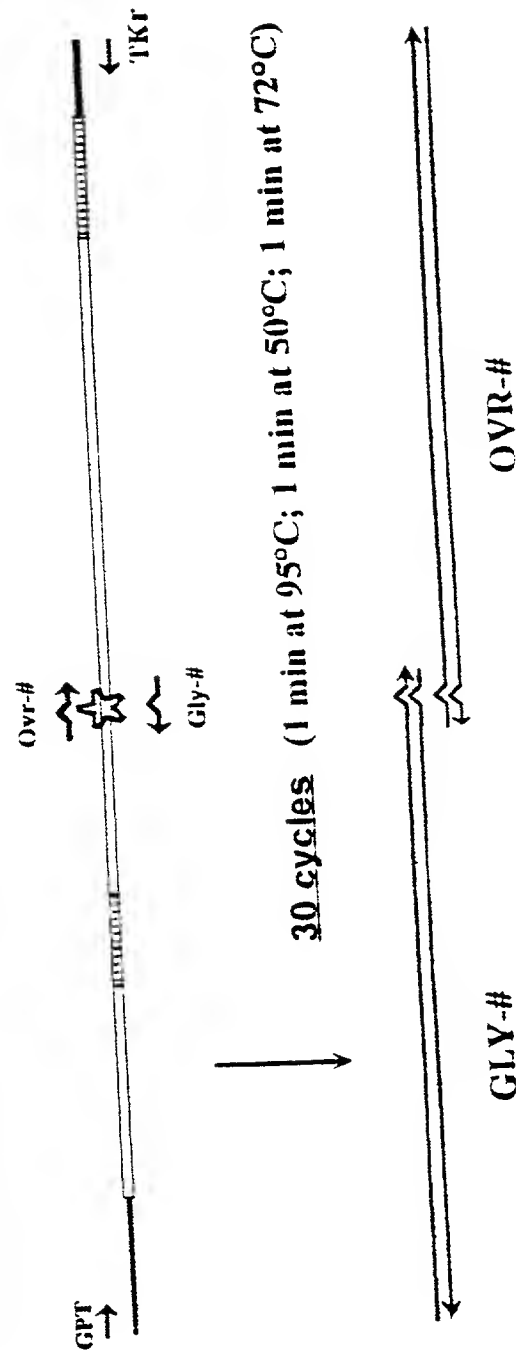


Fig. 42A *In Vitro* Mutagenesis of HCV E1 glycoprotein



1. First step of PCR amplification (Gly-# and Ovr-# primers)



2. Overlap extension and nested PCR

Fig. 42B

a. Overlap extension

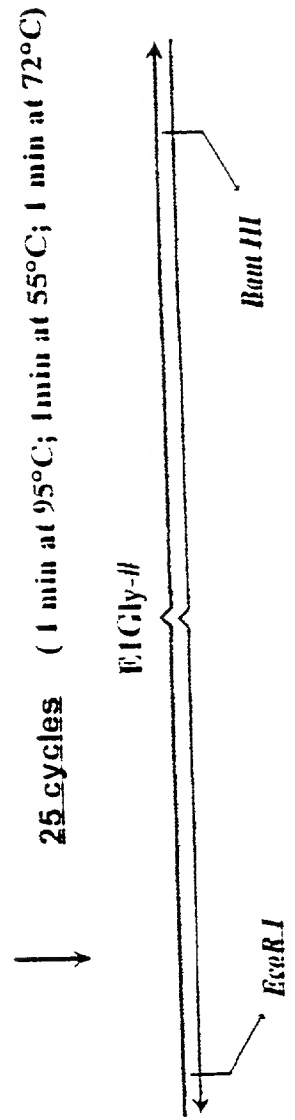
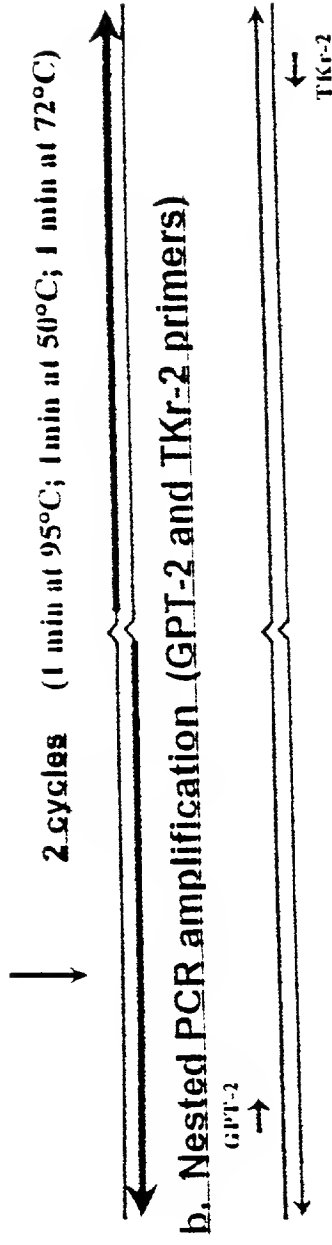
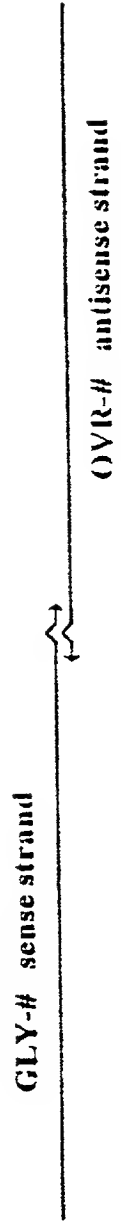
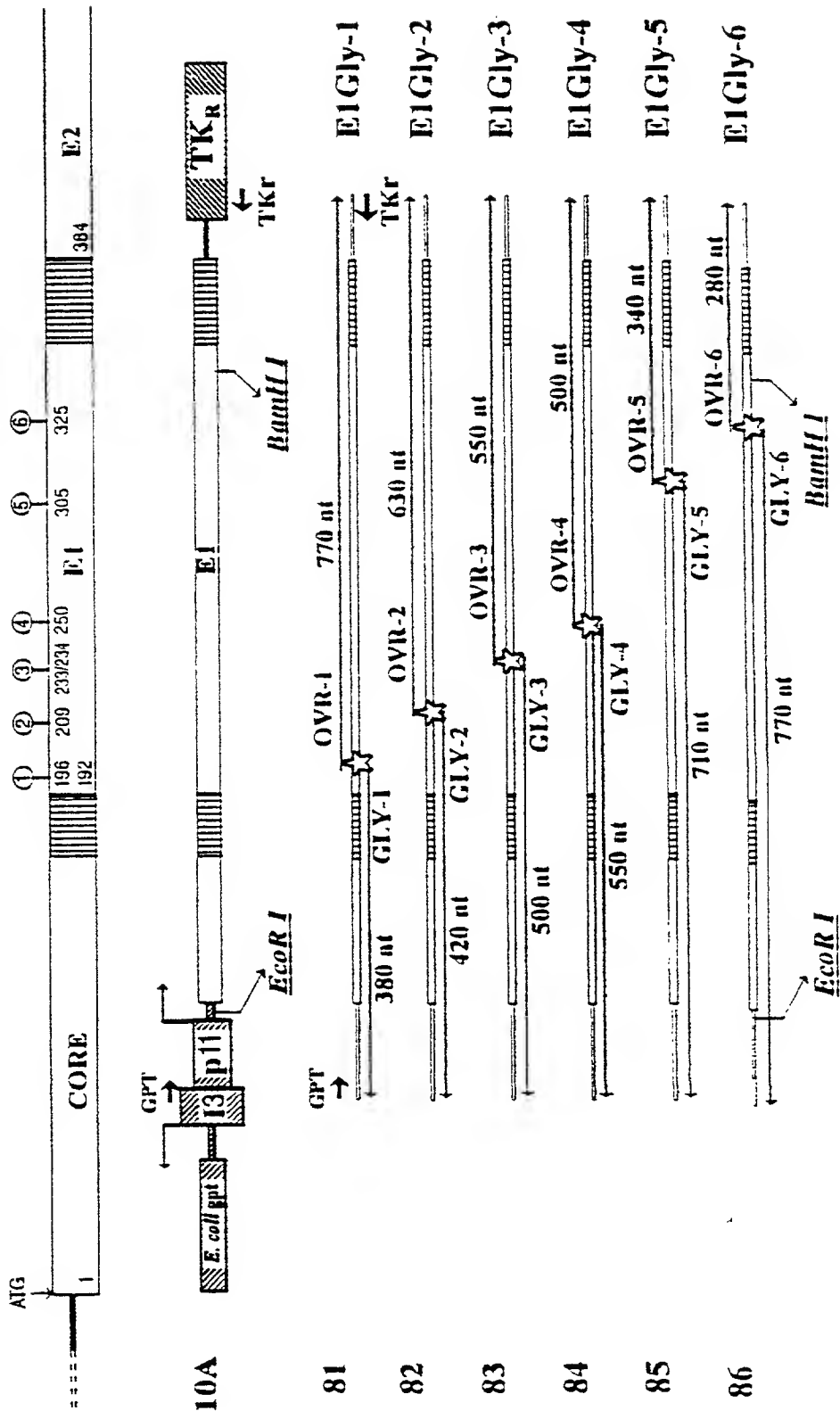


Fig. 43 *In Vitro* Mutagenesis of IICV E1 glycoprotein



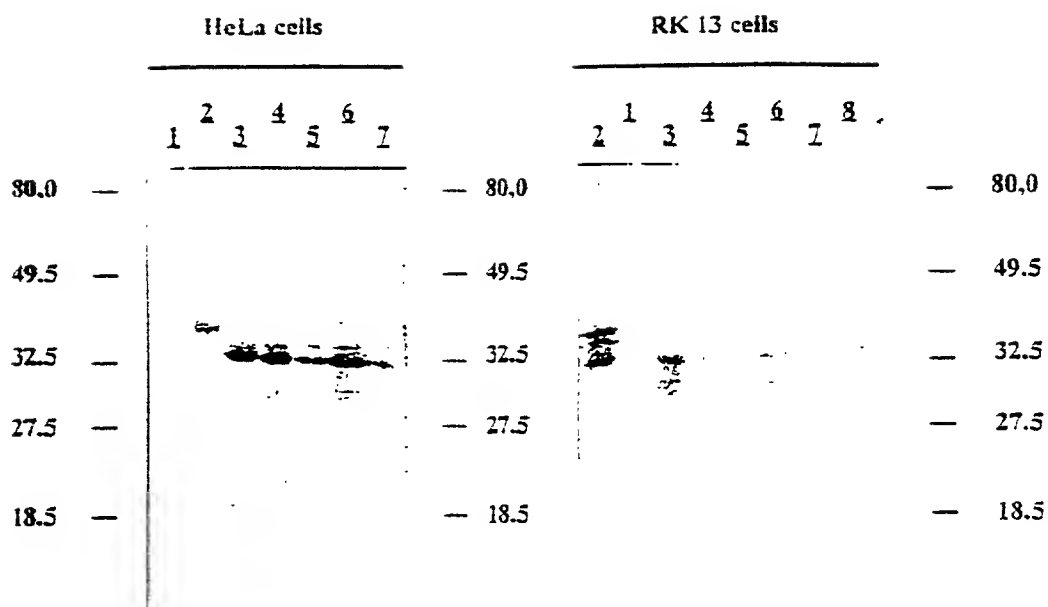


Fig.44A

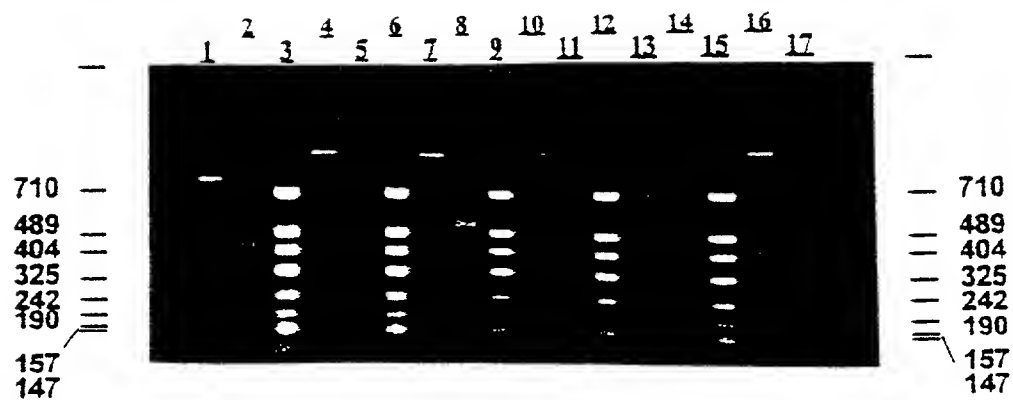


Fig.44B



Fig. 45

KDa 119 67 43 29 18

| | | | |



Fig. 46

Fig. 47

	age (years)	HCV infection (years)	genotype
Marcel	17	9	1a
Peggy	21	16.5	1b
Fenna	15	9	1a
Yoran	12	none	
Marti	12	none	

chronic carriers (strong T-cell adjuvant)

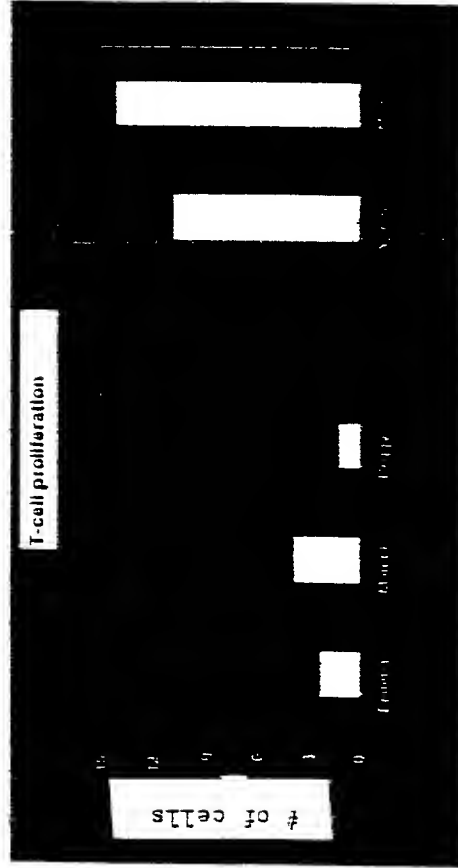
↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ 50 µg E1 dose
 0 3 6 9 12 15 26 29 32 35 38 41 weeks

naive (alum)

↓ ↓ ↓ ↓ ↓ ↓ 50 µg E1 dose
 0 3 6 9 12 15 weeks

Fig. 48

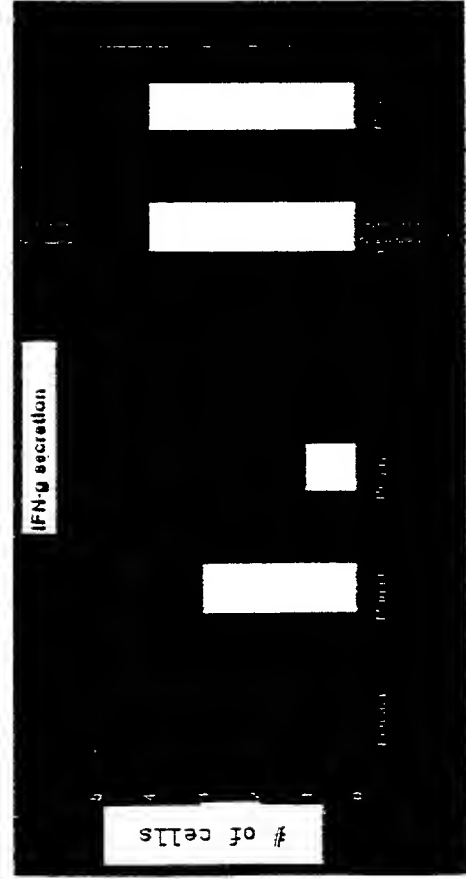
48a



48b



48c



48d

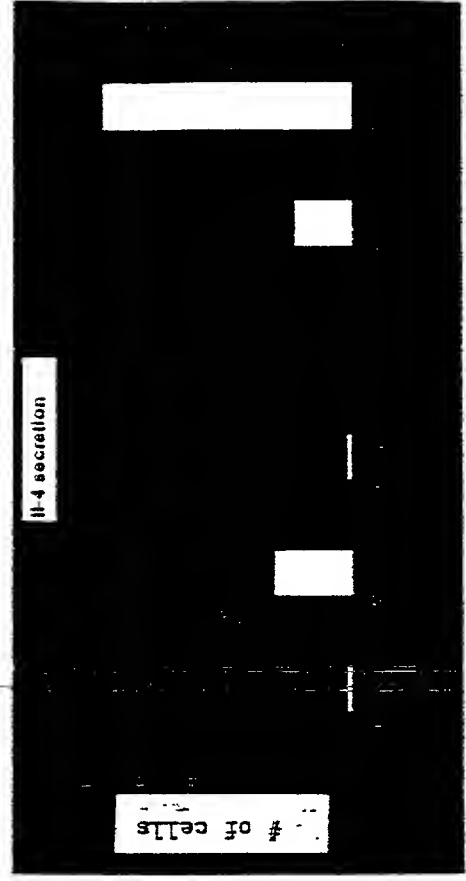
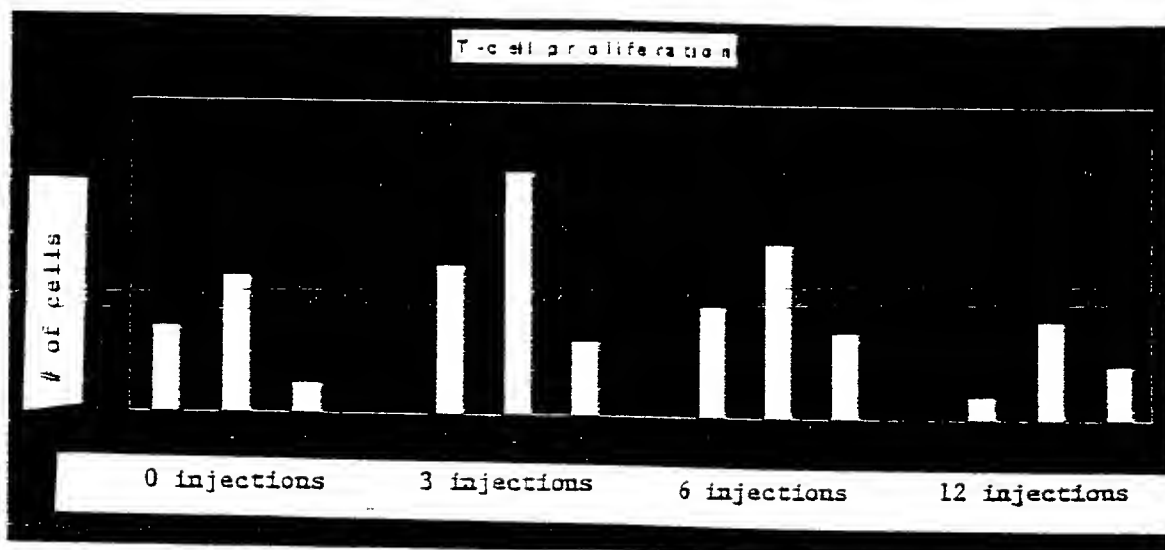


Fig. 49



1 Fem m a, 2 Marcel, 3 Peggy

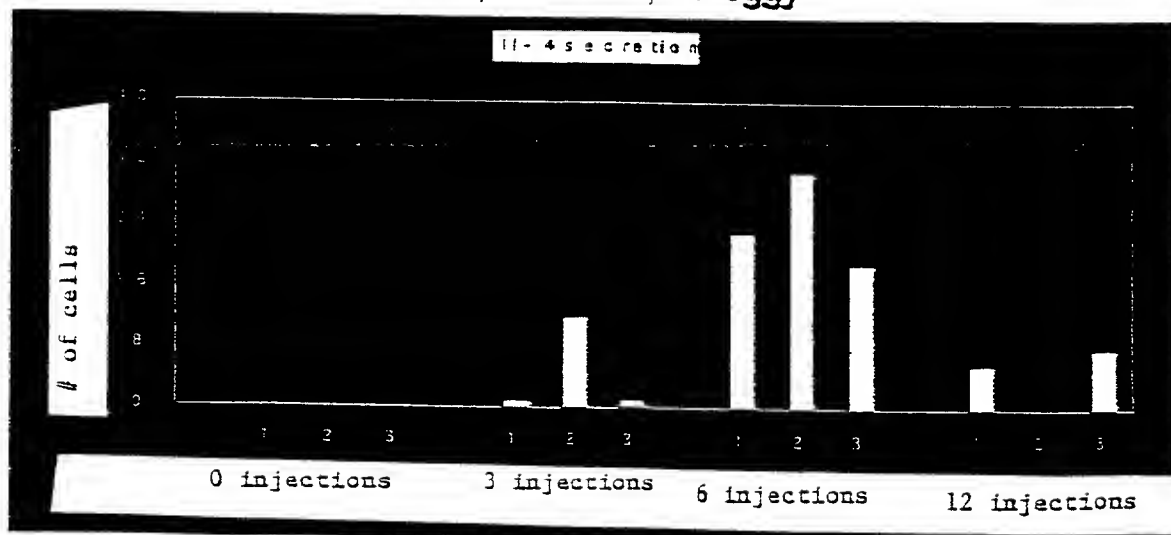
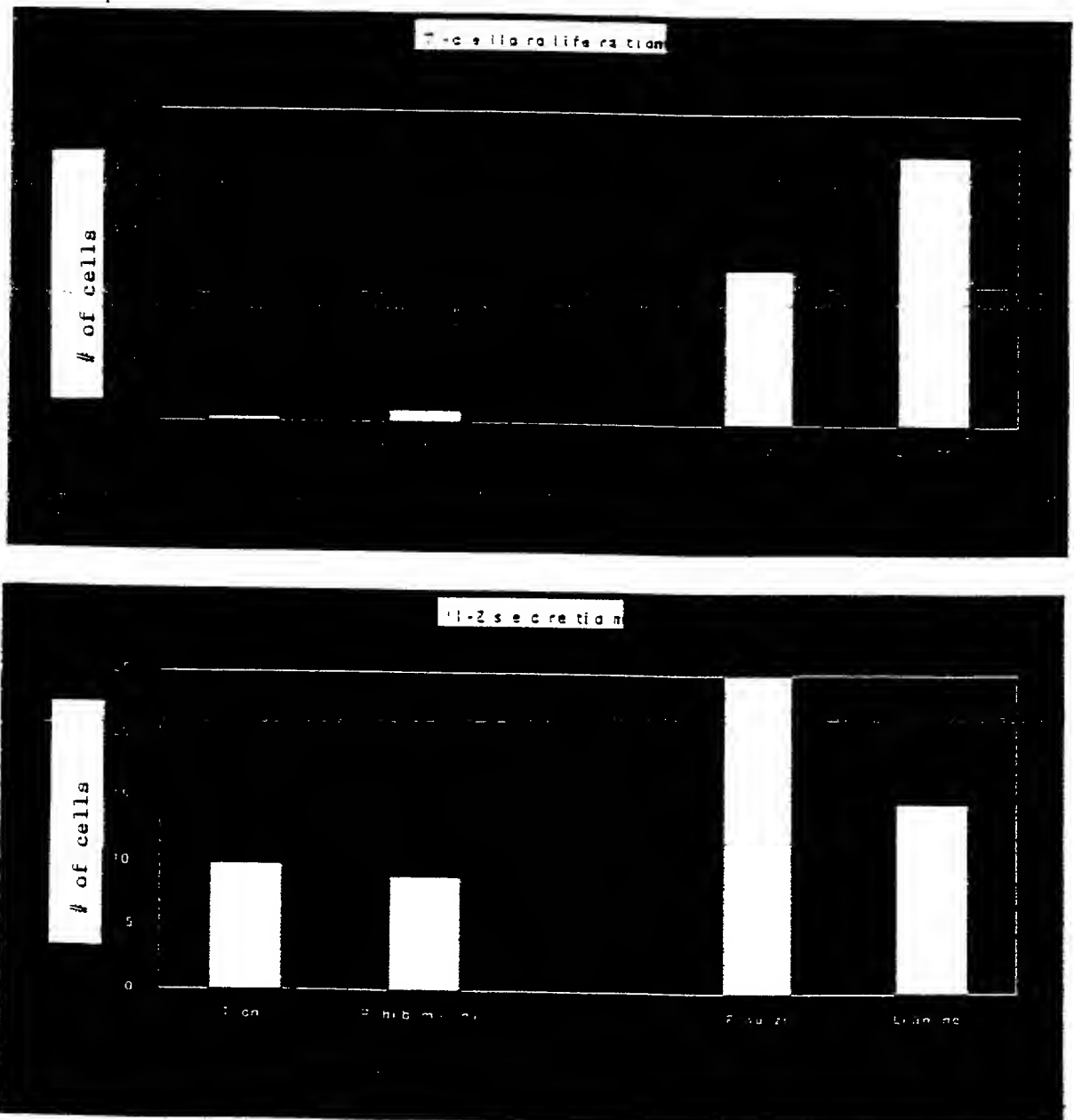


Fig. 50



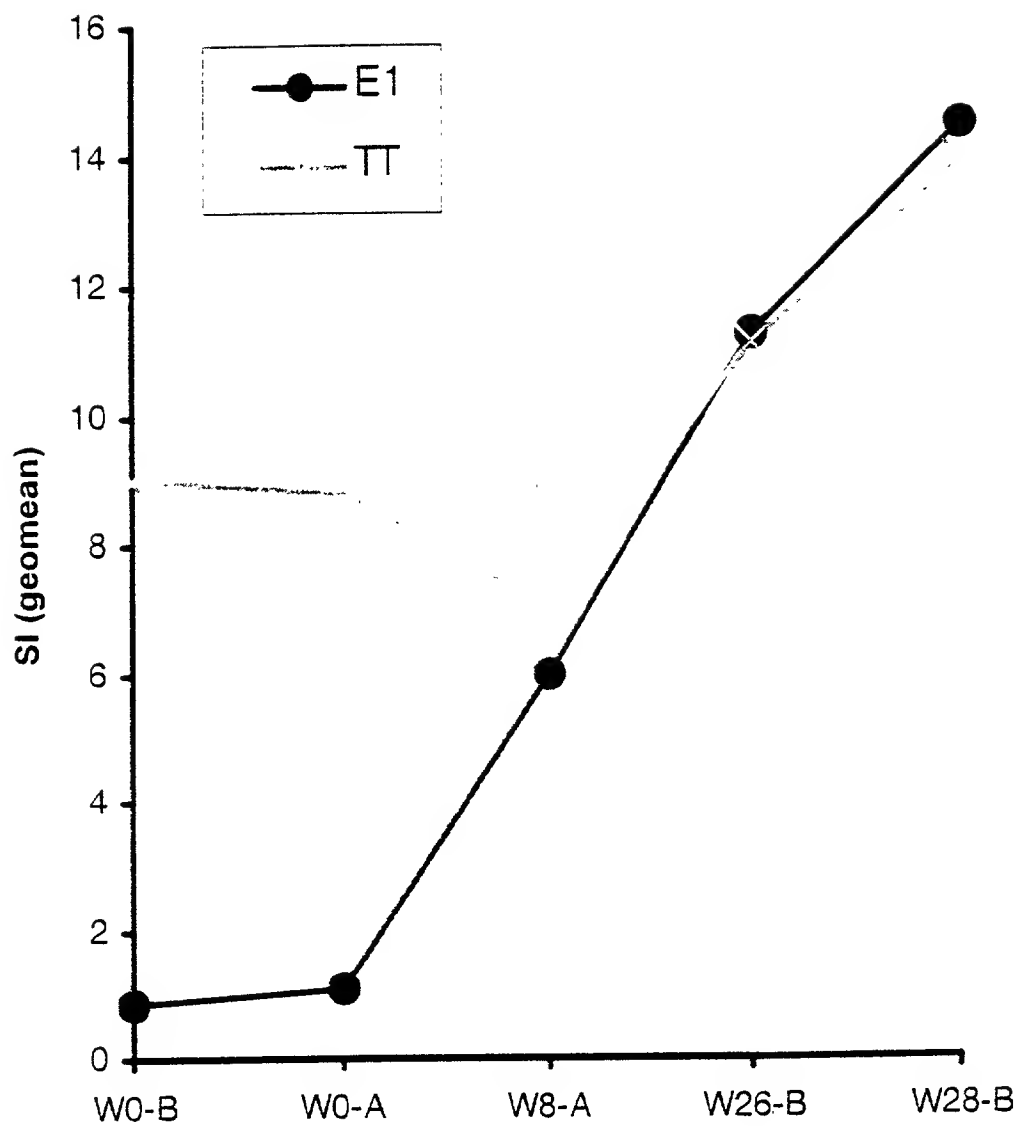


Fig 51

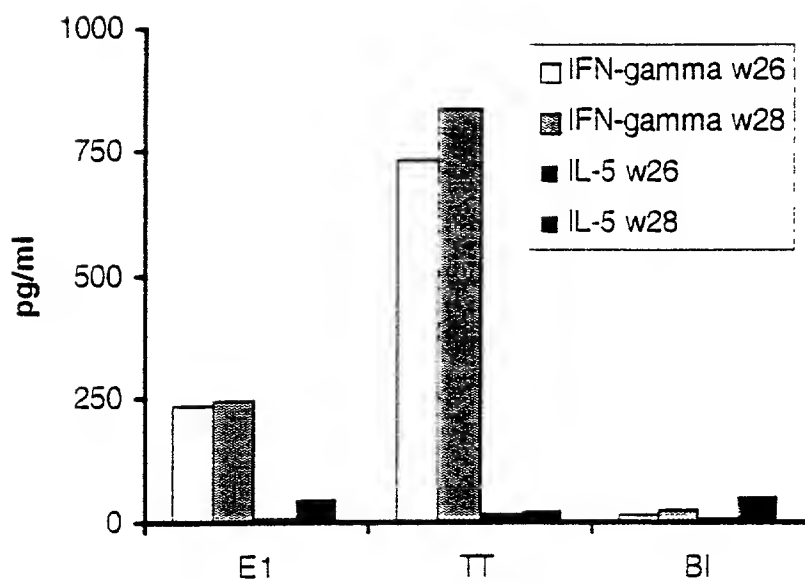


Fig 52

[illegible]